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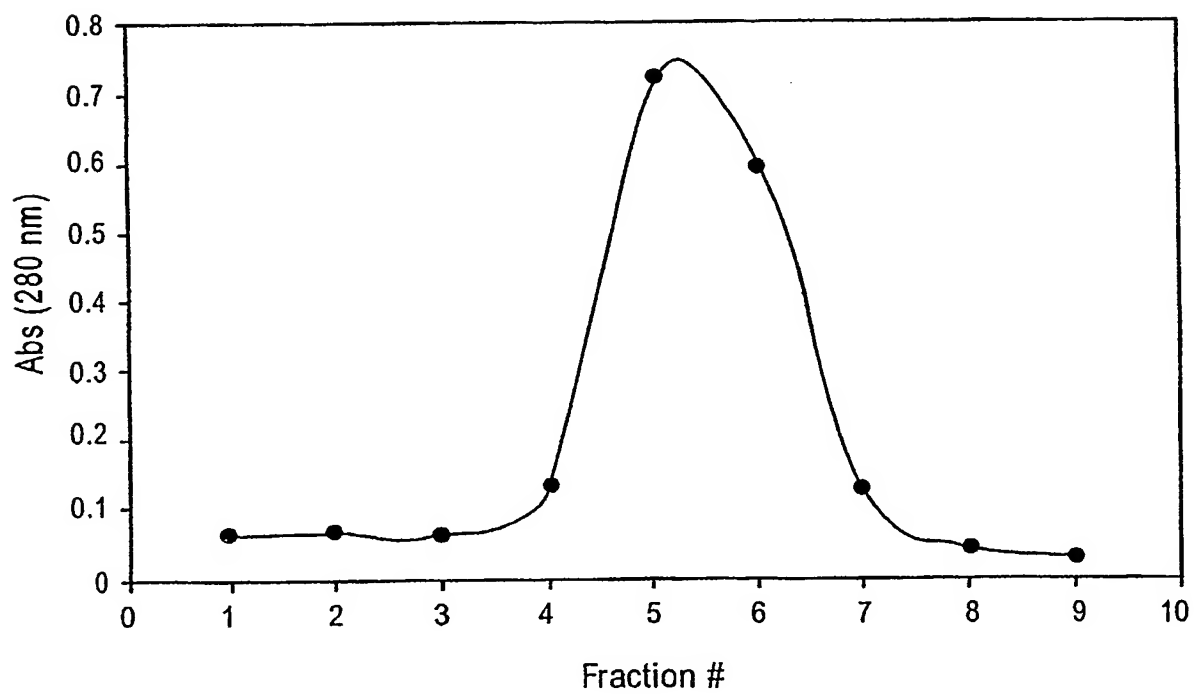
	1 mM	0.1 mM	0.3 mM	mM	mM	0.055%	550 mM	1.1 mM	2.2 mM	2.2 mM	440 mM	550 mM	Activity
#	GSH	GSSG	LM	NaCl	KCl	PEG 3350	GndHCl	EDTA	MgCl <sub>2</sub>	CaCl <sub>2</sub>	Sucrose	L- Arg	U/g IB
2 (55 mM MES pH 6.5)	+	+	+	10.56	0.44	0	+	0	+	+	0	0	0
3 (55 mM MES pH 6.5)	+	+	0	10.56	0.44	+	+	+	0	0	+	+	0
#5 (55 mM MES pH 6.5)	+	+	0	264	11	0	0	0	+	+	+	0	0
#8 (55 mM MES pH 6.5)	+	+	+	264	11	+	0	+	0	0	0	+	40.00
#10 (55 mM MES pH 8.2)	+	+	+	10.56	0.44	0	0	+	0	0	+	0	0
#11 (55 mM Tris pH 8.2)	+	+	0	10.56	0.44	+	0	0	+	+	0	+	105.26
#13 (55 mM Tris pH 8.2)	+	+	0	264	11	0	+	+	0	0	0	0	15.65
#16 (55 mM Tris pH 8.2)	+	+	+	264	11	+	+	0	+	+	+	+	48.70

FIG. 1

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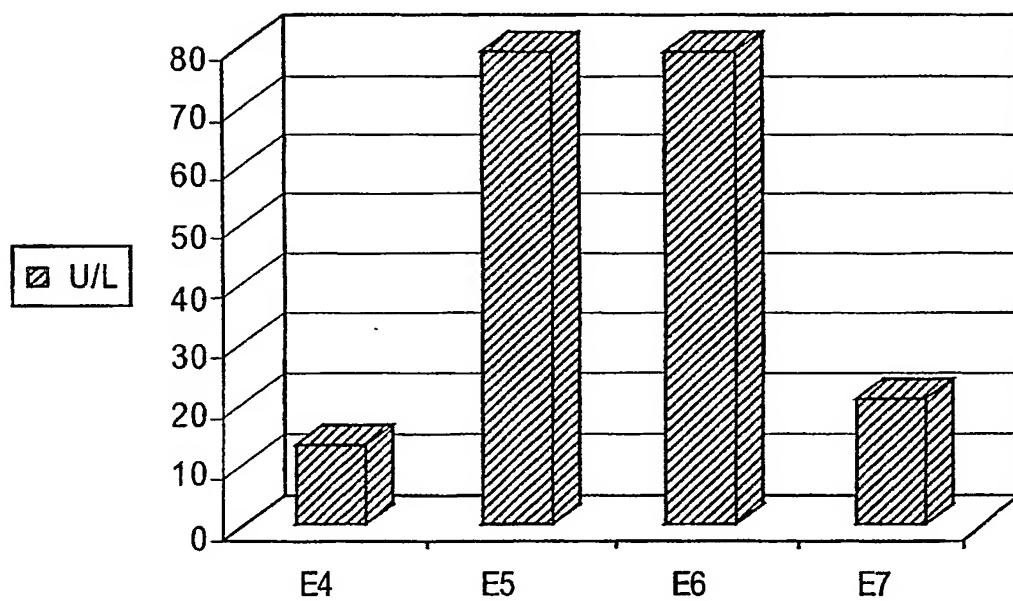
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## ELution of MBP-ST3Gal III from Amylose column

**FIG. 2**

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**ST3 Gal III activities of the Amylose purified  
refolded MBP-ST3Gal III fractions**

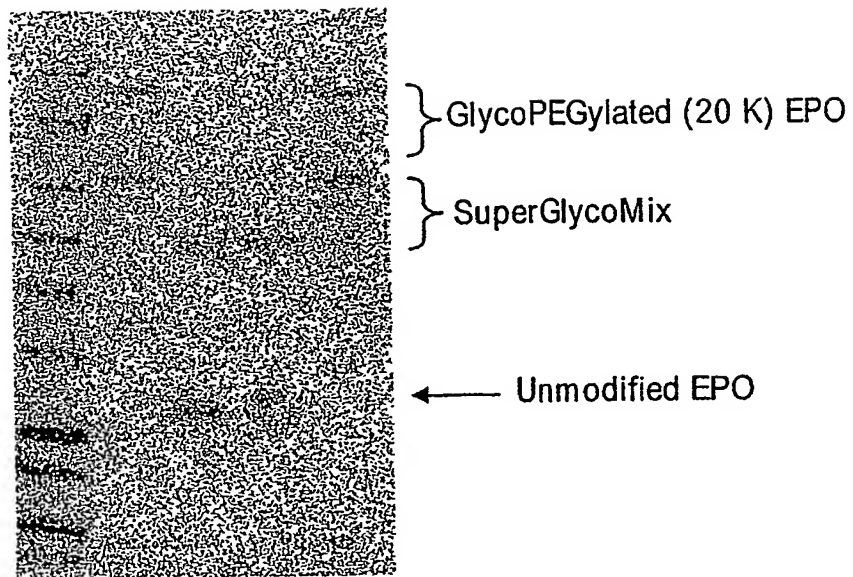


**FIG. 3**

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**FIG. 4**

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GlycoPEGylation (20 K) of EPO

**FIG. 5**

10 20 30 40 50 60  
/usr/t MLKKQSAGLV LWGAILFVAWNA LLLFFWTRPAPGRPPSVSALDGD PASLTREVI RLAQD  
::: ::  
P27115 MLKKQSAGLV LWGAILFVAWNA LLLFFWTRPVPSRL PSDNALDDDPASLTREVI RLAQD

10 20 30 40 50 60  
70 80 90 100 110  
/usr/t AEVELERQRGLLQQIGD--ALSSQRGRVPTA APPAQPRVFVTPAPA VIPILVIACDRSTV  
::: : ::  
P27115 AEVELERQRGLLQQIREH HALWSQRWKVP TAAPPAPHVPVTPPPAVIPILVIACDRSTV

70 80 90 100 110 120  
120 130 140 150 160 170  
/usr/t RRCLDKLLHYRPSAE LFPIIVSQDCGHEETAQA IASYGS AVTHIRQPDLSSI AVPPDHRK  
:::  
P27115 RRCLDKLLHYRPSAE LFPIIVSQDCGHEETAQV IASYGS AVTHIRQPDL SNI AVQPDHRK

130 140 150 160 170 180  
180 190 200 210 220 230  
/usr/t FQGYYKIARHYRWAL GQVFRQFRPA AAVVEDDLE VAPDFFEY FRATYP LLKADPSL WCV  
:::  
P27115 FQGYYKIARHYRWAL GQIFHNFNYP AA VVEDDLE VAPDFFEY FQATYP LLKADPSL WCV

190 200 210 220 230 240  
240 250 260 270 280 290  
/usr/t SAWNDNGKEQMVDAS RP ELLYRTDFF PGLGWLL LAELWAE LE PKWP KAFWD DDMRRPE QR  
:::  
P27115 SAWNDNGKEQMVD SS KP ELLYRTDFF PGLGWLL LAELWAE LE PKWP KAFWD DDMRRPE QR

250 260 270 280 290 300  
300 310 320 330 340 350  
/usr/t QGRACIRPEISRTMT FG RKGVSHGQFFDQH LKF IKLNQQF VHFTQLDLSYLQ REAYDRDF  
:::  
P27115 KGRACVRPEISRTMT FG RKGVSHGQFFDQH LKF IKLNQQF VPFTQLDLSYLQ QEAYDRDF

310 320 330 340 350 360  
360 370 380 390 400 410  
/usr/t IARVYGAPQLQVEKV RTNDRKELGE VRVOYTGRDS FKAFAKALGMDDLKSGV PRAGYRG  
:::  
P27115 IARVYGAPQLQVEKV RTNDRKELGE VRVOYTGRDS FKAFAKALGMDDLKSGV PRAGYRG

370 380 390 400 410 420  
420 430 440  
/usr/t IVTFQFRGRRVHL APPTWEGYDPSWN  
::::  
P27115 IVTFLFRGRRVHL APQTWDGYDPSWT

430 440

FIG. 6

FIG. 6

## GnT1 Cys121Ser mutant

avipilviacdrstvrrslkillhyrpsaelfpfiivvsqdcgheetaqaiasygsavthirqpdlssiaavpdpnrkfggyykiarhyrwa  
lgqvfrqfrfpaavvddleavpddfeyfratypilkadpslwcvswndnkeqmvdasrpeilyrtddfpjgllaelwae  
lepkwpkafvddwmrpeqrqgracirpeisrtmtfgrkgsbqgffdqhlkfiklnqfvlhftqldisylqreaydrdflarvyg  
apqlqvekvrtndrkelgevrvqytrdsfkafakalgvmddlksgvpragyrivtfqfpgtrrvhlappptwegydpwn\*

[illegible]





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## GnT1 Cys121Thr

avipilviacdrstvrtdklilhypsaelfpiivsqdcgheetaqaiasygsavthirqpdlssiaavppdhrkfqgyykiarhyrwal  
 ggqvfqrfrfpaavvveddleavpddffeyfratypilkadpslwcvswndngkeqmvdasrpellyrtdffpglgwllaelwael  
 epkwpkafwddwmrpeqrqgracirpeisrmtfgrkgsvshgqffdqhlkfiklnqqfwhftqlldlsylqreaydrdflarvyg  
 apqlqvekvtrndrkelgevrvqvtgrdsfkafakalgvmddlksvpragyrqivtfqfpgrrvhlappptwegydpawn\*

Gcgggtattcccatcctgtgcatcgccctgtgaccgcagcaactgttcggcgcactctagacaagctgctgcattatcgccctcggctg  
 agctottcccatcatcggttagccaggaactgcgggcacgaggagacggcccaggccatcgctctactaggcagcgcgggtcacgcac  
 atccggcagccccgacctgagcagcattgcggcgccggaccaccgcaagttccagggttactactacaagatcgccggccactacc  
 gctggggcgctggggccaggtcttccggcaggttctgcttcccccggccggtggtggagagatgacctggagggtggccccggacttct  
 tcgagttactttcggggccacctatccgctgctgaaaggccgacccctcctgtgtgctgctcggcctgggaatgacaaacggcaaggagc  
 agatgggtggacggccagcctgagctgctctaccgcacggacttttccctggcctggggctggctggtgtggcaggctctggggc  
 tgagctggagagcccaagtgggccaaaggcccttctgggacgactggatgcggcgccggcagcagggcgaggccctgcatac  
 gccctgagatctcaagaacgagatgaccttggcccgcaagggtgtgagccacggcgagttcttgaccagcacctcaagtttatcaagctg  
 aaccagcagtttgtgcacttcaaccagctggacctggacctgtcttacctgacagcggggagccctatgacaggatttctcgcgcgtctacggg  
 tgcctcccccagctgcaggtggagaaagtggagaccaatgaccggaaaggagctgggggagagctgcgggtgcagtatacggggcaggsga  
 cagcttcaaggcttccgcaaggctctgggtgtcatgagatgacctaaagtccgggggtccgagagagctggctacccgggggtattgtcacctt  
 ccagttcccgggcccgctgtgtccacctggcgccccccaccgacgtggggagggtctatgacatcctagctgggaattag

FIG. 9

## GnT1 Cys121Ala

avipilviacdrstvrraldkllhyrpsaelfpiivsqdcgheetaqiaasygsavthirqpdlssiaavppdhrkfqgvykiarhyrwa  
lgvqfrqfrpaavvdedlevapdffeyfratypllkadpslwcvswndngkeqmvdasrpellyrtddfpglgwllaelwae  
lepkwpkafwdwmrpeqrqgracirpeisrtmtfgrkgvshgqfddqhlkfiknqfvehftqldisylqreaydrdrflarvyg  
apqlqvekvrtndrkelgevrvqytdrdsfkafakalgvmddlksgvpragyrvtfqfgrvrlhappptwegydpswn\*

[illegible]

**FIG. 10**

## GnT1 Arg120Ala, Cys121H

avipilviacdtrstvr**ah**ldklhlyrpsaelfiivsqdcgheetaqaiasygsavthirqpdlssiaavppdhrkfqgyykiarhyrw  
algvvfqrqfrfpaavvdedlevapdffeyfratypilkadpslwcvswndngkeqmvdasrpellyrtddffglgwllaelwa  
elepkwpkafwdwmrpeqrqgracirpeistmtfgrkgvshgffdqhlkfiklnqcfvhtfqldlsylqreaydrdrflarvy  
gapqlqvekvitndrkelgevrvqytgrdsfkafakalgvmddlksvpragyrgivtfqfpgrrvhlappptwegydp<sup>swn</sup>\*

Gcggigfgrattoccatocfgrfgrtcatocgocfgrfgracogacatfgrtgrggrccacccatagacaaagctgrtgrcattatocggrccctcgrggrctgr  
agctcttcccatcatcctgrfgrtagccacggrgactgrccgrgacacggrgagagccggrccacaggrccatcctctctatcgrgacgocgocgrgtcatcagccac  
atccgrgacgcccgracotgragcagcattgrggrtgrccgocggrgacacocgacaaagrttccacggrgcttactatcaagagatocgocgocacatcac  
grtgrggrcgrctgrggrccacggrtcttccgrgacagrttccgrtcccccgrggrcccggrfgrgrgrtgrgaggrgratgracotgrggrggrcccccgrggractct  
tcgrgagrtacttccgrggrccacatcatccgrctgrctgrgaggrgcccgrgaccccctccctgrfgrgrtgrctcgrggrccctgrggrgagrtgacaaacggrgcaaggrgagoc  
agratgrgrgrgacgcccacagocaggrccctgraggrctgrctctatccgrgacccagratfrrtccctgrggrccctgrggrctgrctgrtgrgrccctgrggrcc  
tgraggrctgrgaggrccacaaagrtgrgcccagaggrccctfctgrggrgacgratgrgrgrtgrcgrggrccggrgagocggrgacggrgaggrggrccctgrcataac  
gcccgrgagratcatagaaagacgagatgracctfgrggrccgrcagaggrgrgrgrgacacggrggrgagrttctfrrgacacaggracacctcaagrttctatcaaggrctgr  
aaacagcaggrfrrgrgacatfcaocccagctgrggracotgrtcttaccctgrcagocgrggraggrccctatgracocaggratfrrtccctcgrcccgctctacggr  
tgrctccacagctgrcaggrtgrgaggrgaaagrtgraggrgrgacacaaatgracocgrgaaaggraggrctgrgrgrgrgaggrtataccgrggrcaggrggrga  
cagrttcaaggrgcttccgcccagaggrctctgrgrgrtctcatgrgagatgracacftaaagrtcgrggrgrtcccgaggraggrctgrggrtacccgrggrgrtattgrtcaacct  
ccagrttcccggrggrcccggrtgrtccacacotgrggrcccccacccaggracgrgrgrgrggrggrctatgratcctatgrctgrggrgaaatag

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**FIG. 11**

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## Rat Liver ST3Gal III amino acid sequence:

MGLLVFVVRNLLALCLFLVLGFLYYSAMKLHLLQWEDSNLILSLDSAGQTLGTEYDRL  
 GFLKLLDSKLPaelATKyanfSEGACKPGYASAMMTAIFPRFSKPAPMFLDDSFRRKW  
 ARIRFVPPFGIKGQDNLIKAILSVTKYRLTPALDSLHCRRCIIVGNGGVLANKSLGS  
 RIDDYDIVIRLNSAPVKGFEKDVGSKTTLRITYPEGAMQRPEQYERDSLFLAGFKW  
 QDFKWLKYIVYKERVASDGFWKSVATRPKEPPEIRILNPYFIQEAFTLIGLPFNN  
 GLMGRGNPTLGSVAVTMALDGCDEVAVAGFGYDMNTPNAPLHYETVVRMAAIKE  
 SWTHNIQREKEFLRKLVKARVITDLSSGI

FIG. 12

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**Full length UDP-N-acetylgalactosaminyltransferase 2 (GalNAcT2)****nucleic acid and amino acid sequences****Amino acid sequence**

Met	Arg	Arg	Arg	Ser	Arg	Met	Leu	Leu	Cys	Phe	Ala	Phe	Leu	Trp	Val
1				5					10					15	
Leu	Gly	Ile	Ala	Tyr	Tyr	Met	Tyr	Ser	Gly	Gly	Gly	Ser	Ala	Leu	Ala
			20					25					30		
Gly	Gly	Ala	Gly	Gly	Gly	Ala	Gly	Arg	Lys	Glu	Asp	Trp	Asn	Glu	Ile
		35					40					45			
Asp	Pro	Ile	Lys	Lys	Lys	Asp	Leu	His	His	Ser	Asn	Gly	Glu	Glu	Lys
	50					55					60				
Ala	Gln	Ser	Met	Glu	Thr	Leu	Pro	Pro	Gly	Lys	Val	Arg	Trp	Pro	Asp
65					70					75					80
Phe	Asn	Gln	Glu	Ala	Tyr	Val	Gly	Gly	Thr	Met	Val	Arg	Ser	Gly	Gln
				85					90					95	
Asp	Pro	Tyr	Ala	Arg	Asn	Lys	Phe	Asn	Gln	Val	Glu	Ser	Asp	Lys	Leu
			100					105					110		
Arg	Met	Asp	Arg	Ala	Ile	Pro	Asp	Thr	Arg	His	Asp	Gln	Cys	Gln	Arg
		115					120					125			
Lys	Gln	Trp	Arg	Val	Asp	Leu	Pro	Ala	Thr	Ser	Val	Val	Ile	Thr	Phe
	130					135					140				
His	Asn	Glu	Ala	Arg	Ser	Ala	Leu	Leu	Arg	Thr	Val	Val	Ser	Val	Leu
145					150					155					160
Lys	Lys	Ser	Pro	Pro	His	Leu	Ile	Lys	Glu	Ile	Ile	Leu	Val	Asp	Asp
				165					170					175	
Tyr	Ser	Asn	Asp	Pro	Glu	Asp	Gly	Ala	Leu	Leu	Gly	Lys	Ile	Glu	Lys
			180					185					190		
Val	Arg	Val	Leu	Arg	Asn	Asp	Arg	Arg	Glu	Gly	Leu	Met	Arg	Ser	Arg
		195					200					205			
Val	Arg	Gly	Ala	Asp	Ala	Ala	Gln	Ala	Lys	Val	Leu	Thr	Phe	Leu	Asp
	210					215					220				
Ser	His	Cys	Glu	Cys	Asn	Glu	His	Trp	Leu	Glu	Pro	Leu	Leu	Glu	Arg
225					230					235					240
Val	Ala	Glu	Asp	Arg	Thr	Arg	Val	Val	Ser	Pro	Ile	Ile	Asp	Val	Ile
				245					250					255	
Asn	Met	Asp	Asn	Phe	Gln	Tyr	Val	Gly	Ala	Ser	Ala	Asp	Leu	Lys	Gly
			260					265					270		
Gly	Phe	Asp	Trp	Asn	Leu	Val	Phe	Lys	Trp	Asp	Tyr	Met	Thr	Pro	Glu
		275					280					285			

**FIG. 13A**

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Gln	Arg	Arg	Ser	Arg	Gln	Gly	Asn	Pro	Val	Ala	Pro	Ile	Lys	Thr	Pro
290						295					300				
Met	Ile	Ala	Gly	Gly	Leu	Phe	Val	Met	Asp	Lys	Phe	Tyr	Phe	Glu	Glu
305					310					315					320
Leu	Gly	Lys	Tyr	Asp	Met	Met	Met	Asp	Val	Trp	Gly	Gly	Glu	Asn	Leu
				325					330					335	
Glu	Ile	Ser	Phe	Arg	Val	Trp	Gln	Cys	Gly	Gly	Ser	Leu	Glu	Ile	Ile
			340					345					350		
Pro	Cys	Ser	Arg	Val	Gly	His	Val	Phe	Arg	Lys	Gln	His	Pro	Tyr	Thr
		355					360					365			
Phe	Pro	Gly	Gly	Ser	Gly	Thr	Val	Phe	Ala	Arg	Asn	Thr	Arg	Arg	Ala
	370					375					380				
Ala	Glu	Val	Trp	Met	Asp	Glu	Tyr	Lys	Asn	Phe	Tyr	Tyr	Ala	Ala	Val
385					390					395					400
Pro	Ser	Ala	Arg	Asn	Val	Pro	Tyr	Gly	Asn	Ile	Gln	Ser	Arg	Leu	Glu
				405					410					415	
Leu	Arg	Lys	Lys	Leu	Ser	Cys	Lys	Pro	Phe	Lys	Trp	Tyr	Leu	Glu	Asn
			420					425					430		
Val	Tyr	Pro	Glu	Leu	Arg	Val	Pro	Asp	His	Gln	Asp	Ile	Ala	Phe	Gly
		435					440					445			
Ala	Leu	Gln	Gln	Gly	Thr	Asn	Cys	Leu	Asp	Thr	Leu	Gly	His	Phe	Ala
		450				455					460				
Asp	Gly	Val	Val	Gly	Val	Tyr	Glu	Cys	His	Asn	Ala	Gly	Gly	Asn	Gln
465					470					475					480
Glu	Trp	Ala	Leu	Thr	Lys	Glu	Lys	Ser	Val	Lys	His	Met	Asp	Leu	Cys
				485					490					495	
Leu	Thr	Val	Val	Asp	Arg	Ala	Pro	Gly	Ser	Leu	Ile	Lys	Leu	Gln	Gly
			500					505					510		
Cys	Arg	Glu	Asn	Asp	Ser	Arg	Gln	Lys	Trp	Glu	Gln	Ile	Glu	Gly	Asn
		515					520					525			
Ser	Lys	Leu	Arg	His	Val	Gly	Ser	Asn	Leu	Cys	Leu	Asp	Ser	Arg	Thr
	530					535					540				
Ala	Lys	Ser	Gly	Gly	Leu	Ser	Val	Glu	Val	Cys	Gly	Pro	Ala	Leu	Ser
545					550					555					560
Gln	Gln	Trp	Lys	Phe	Thr	Leu	Asn	Leu	Gln	Gln					
				565					570						

**FIG. 13A (CONT.)**  
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Nucleic acid sequence

atgogggggc gctoggggat gctgctctgc ttogocttoc tgtgggtgct gggcatogoc	60
tactacatgt actogggggg cggctctgog ctggocgggg gogggggogg oggogggggc	120
aggaaggagg actggaatga aattgaoccc attaaaaaga aagaocctca tcacagcaat	180
ggagaagaga aagcacaaag catggagac ctocctocag ggaagtaog gtggocagac	240
tttaaccagg aagcttatgt tggagggag atggtocgct cggggcagga oocttaogoc	300
ogcaacaagt tcaacagggt ggagagtgat aagcttogaa tggacagagc catocctgac	360
acccggcatg aocagtgta ggggaagcag tggoggggtgg atctgocggc caccagcgtg	420
gtgatcaggt ttcacaatga agocaggto ggcactactca ggaocgtggc cagcgtgctt	480
aagaaaagoc cggccatct cataaaaaga atcatcttgg tggatgacta cagcaatgat	540
octgaggag gggctctctt ggggaaaatt gagaaagtgc gagttcttag aaatgatoga	600
ogagaaggoc tcatgogctc acgggttogg ggggocgatg ctgoccaagc caaggtocgt	660
aocctocgtg acagtcactg cagtgtaat gagcactggc tggagococ octggaaagg	720
gtggoggagg acaggactog ggttggtgca cccatcatog atgtcattaa tatggacaac	780
tttcagtatg tgggggcac tgcagacttg aagggcgggt ttgattggaa cttggtattc	840
aagtgggatt acatgaogoc tgagcagaga aggtocggc aggggaoc agtogococ	900
ataaaaaoc ccatgattgc tgggtgggctg tttgtgatgg ataagttcta ttttgaagaa	960
ctggggaagt acgacatgat gatggatgtg tggggaggag agaocctaga gatctogttc	1020
cggtgtggc agtgtggtgg cagocggag atcatocgct gcagocgtgt gggacacgtg	1080
ttocggaagc agcaccocca cccgttcccg ggtggcagtg gcactgtctt tgcccgaaac	1140
acccggogg cagcagagggt ctggatggat gaatacaaaa atttctatta tgcagcagtg	1200
occtctgcta gaaocgttcc ttatggaaat attcagagca gattggagct taggaagaaa	1260
ctcagctgca agoccttcaa atggtacott gaaaatgtct atocagagtt aagggttoca	1320
gaocatcagg atatagcttt tggggocctg cagcagggaa ctaactgoc octacacttg	1380
ggacacttg ctgatggtgt ggttggagtt tatgaatgtc acaatgctgg gggaaacag	1440
gaatgggoc tgaogaagga gaagtoggtg aagcacatgg atttgtgoc tactgtggtg	1500
gaocgggcac cggctctct tataaagctg cagggtgoc gagaaaatga cagcagacag	1560
aaatgggaac agatcgaggg caactocaag ctgaggcag tgggcagcaa octgtgocgtg	1620
gacagtogca cggocaagag cgggggocca agcgtggagg tgtgtggoc ggcoccttgg	1680
cagcagtgga agttcagcct caaocctgag cag	1713

**FIG. 13B**  
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**Δ51 UDP-N-acetylgalactosaminyltransferase 2, GalNAcT2,  
nucleic acid and amino acid sequences**

Amino acid sequence

Lys	Lys	Lys	Asp	Leu	His	His	Ser	Asn	Gly	Glu	Glu	Lys	Ala	Gln	Ser
1				5					10					15	
Met	Glu	Thr	Leu	Pro	Pro	Gly	Lys	Val	Arg	Trp	Pro	Asp	Phe	Asn	Gln
			20					25					30		
Glu	Ala	Tyr	Val	Gly	Gly	Thr	Met	Val	Arg	Ser	Gly	Gln	Asp	Pro	Tyr
		35					40					45			
Ala	Arg	Asn	Lys	Phe	Asn	Gln	Val	Glu	Ser	Asp	Lys	Leu	Arg	Met	Asp
	50					55					60				
Arg	Ala	Ile	Pro	Asp	Thr	Arg	His	Asp	Gln	Cys	Gln	Arg	Lys	Gln	Trp
65					70					75					80
Arg	Val	Asp	Leu	Pro	Ala	Thr	Ser	Val	Val	Ile	Thr	Phe	His	Asn	Glu
			85						90					95	
Ala	Arg	Ser	Ala	Leu	Leu	Arg	Thr	Val	Val	Ser	Val	Leu	Lys	Lys	Ser
			100					105					110		
Pro	Pro	His	Leu	Ile	Lys	Glu	Ile	Ile	Leu	Val	Asp	Asp	Tyr	Ser	Asn
		115					120					125			
Asp	Pro	Glu	Asp	Gly	Ala	Leu	Leu	Gly	Lys	Ile	Glu	Lys	Val	Arg	Val
	130					135					140				
Leu	Arg	Asn	Asp	Arg	Arg	Glu	Gly	Leu	Met	Arg	Ser	Arg	Val	Arg	Gly
145					150					155					160
Ala	Asp	Ala	Ala	Gln	Ala	Lys	Val	Leu	Thr	Phe	Leu	Asp	Ser	His	Cys
				165					170					175	
Glu	Cys	Asn	Glu	His	Trp	Leu	Glu	Pro	Leu	Leu	Glu	Arg	Val	Ala	Glu
			180					185					190		
Asp	Arg	Thr	Arg	Val	Val	Ser	Pro	Ile	Ile	Asp	Val	Ile	Asn	Met	Asp
		195					200					205			
Asn	Phe	Gln	Tyr	Val	Gly	Ala	Ser	Ala	Asp	Leu	Lys	Gly	Gly	Phe	Asp
	210					215					220				
Trp	Asn	Leu	Val	Phe	Lys	Trp	Asp	Tyr	Met	Thr	Pro	Glu	Gln	Arg	Arg
225					230					235					240
Ser	Arg	Gln	Gly	Asn	Pro	Val	Ala	Pro	Ile	Lys	Thr	Pro	Met	Ile	Ala
				245					250					255	
Gly	Gly	Leu	Phe	Val	Met	Asp	Lys	Phe	Tyr	Phe	Glu	Glu	Leu	Gly	Lys
			260					265					270		
Tyr	Asp	Met	Met	Met	Asp	Val	Trp	Gly	Gly	Glu	Asn	Leu	Glu	Ile	Ser
		275					280					285			
Phe	Arg	Val	Trp	Gln	Cys	Gly	Gly	Ser	Leu	Glu	Ile	Ile	Pro	Cys	Ser

**FIG. 14A**  
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290		295		300
Arg 305	Val	Gly	His	Val
		Phe 310	Arg	Lys
			Gln	His
				Pro 315
				Tyr
				Thr
				Phe
				Pro
				Gly 320
Gly	Ser	Gly	Thr	Val
				Phe 325
				Ala
				Arg
				Asn
				Thr 330
				Arg
				Arg
				Ala
				Ala
				Glu
				Val 335
Trp	Met	Asp	Glu	Tyr
				Lys 340
				Asn
				Phe
				Tyr 345
				Tyr
				Ala
				Ala
				Val
				Pro
				Ser
				Ala 350
Arg	Asn	Val	Pro	Tyr
				Gly 355
				Asn
				Ile
				Gln 360
				Ser
				Arg
				Leu
				Glu
				Leu 365
				Arg
				Lys
Lys	Leu	Ser	Cys	Lys
				Pro 370
				Phe
				Lys 375
				Trp
				Tyr
				Leu
				Glu 380
				Asn
				Val
				Tyr
				Pro 385
Glu	Leu	Arg	Val	Pro
				Asp 390
				His
				Gln
				Asp
				Ile
				Ala 395
				Phe
				Gly
				Ala
				Leu
				Gln 400
Gln	Gly	Thr	Asn	Cys
				Leu 405
				Asp
				Thr
				Leu
				Gly 410
				His
				Phe
				Ala
				Asp
				Gly 415
				Val
Val	Gly	Val	Tyr	Glu
				Cys 420
				His
				Asn
				Ala 425
				Gly
				Gly
				Asn
				Gln
				Glu 430
				Trp
				Ala
Leu	Thr	Lys	Glu	Lys
				Ser 435
				Val
				Lys
				His 440
				Met
				Asp
				Leu
				Cys 445
				Leu
				Thr
				Val 450
Val	Asp	Arg	Ala	Pro
				Gly 455
				Ser
				Leu
				Ile
				Lys
				Leu 460
				Gln
				Gly
				Cys
				Arg
				Glu 465
Asn	Asp	Ser	Arg	Gln
				Lys 470
				Trp
				Glu
				Gln
				Ile
				Glu 475
				Gly
				Asn
				Ser
				Lys 480
Arg	His	Val	Gly	Ser
				Asn 485
				Leu
				Cys
				Leu
				Asp 490
				Ser
				Arg
				Thr
				Ala
				Lys 495
				Ser
Gly	Gly	Leu	Ser	Val
				Glu 500
				Val
				Cys
				Gly 505
				Pro
				Ala
				Leu
				Ser
				Gln 510
				Gln
				Trp
Lys	Phe	Thr	Leu	Asn
				Leu 515
				Gln
				Gln 520

FIG. 14A (CONT.)

## Nucleic acid sequence

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aaaaagaaag	aocttcatca	cagcaatgga	gaagagaaag	cacaaagcat	ggagaoctc	60
octocagggg	aagtaoogtg	gocagacttt	aaocaggaag	cttatgttgg	agggacgatg	120
gtocgctoo	ggcaggaoc	ttacgocgc	aacaagttca	accaggtgga	gagtataag	180
cttogaatgg	acagagoc	oocagacac	oggcagac	agtgtcagcg	gaagcagtg	240
oggttgatc	tgocggcac	cagcgtggg	atcagtttc	acaatgaag	caggtoggc	300
ctactcagga	oogtggtcag	ogtgcttaag	aaaagocgc	occatctcat	aaaagaaac	360
atcttggtgg	atgactacag	caatgatoc	gaggaoggg	ctctcttggg	gaaaattgag	420
aaagtgcgag	ttcttagaaa	tgatogaaga	gaagoccca	tgogctcag	ggttoggggg	480
gocgatgctg	occaagocaa	ggtocagac	ttocggaca	gtcactgoga	gtgtaatgag	540
cactggctgg	agocococ	ggaaagggg	goggaggaca	ggactoggg	tgtgtcaoc	600
atcatogatg	tcattaatat	ggacaacttt	cagtatgtgg	ggcactctgc	tgacttgaag	660
ggoggttttg	attggaactt	ggtattcaag	tgggattaca	tgacgocga	gcagagaagg	720
toocggcagg	ggaococagt	ogococata	aaaacococa	tgattgctgg	tgggctgttt	780
gtgatggata	agttctattt	tgaagaactg	gggaagtacg	acatgatgat	ggatgtgtgg	840
ggaggagaga	aoctagagat	ctogttooc	gtgtggcag	gtggtgccag	oocggagac	900
atocogtgca	gocgtgtggg	acaogtggtc	oggaagcag	aoocacac	gttcooggg	960
ggcagtgcca	ctgtctttgc	ocgaacac	ogocggcag	cagaggtctg	gatggatgaa	1020
tacaaaaatt	tctattatgc	agcagtgoc	tctgctagaa	aocttctta	tggaaatatt	1080
cagagcagat	tggagcttag	gaagaaactc	agctgcaag	cttcaaag	gtaocttga	1140
aatgtctatc	cagagttaag	ggttocagac	catcaggata	tagcttttgg	ggocctgag	1200
caggaacta	actgocoga	cactttggga	cactttgctg	atgggtgtgg	tggagtttat	1260
gaatgtcaca	atgctggggg	aaocaggaa	tgggocctga	ogaaggagaa	gtocgtgaag	1320
cacatggatt	tgtgocctac	tgtgggtggac	oggcacocgg	gctctcttat	aaagctgag	1380
ggctgocgag	aaaatgacag	cagacagaaa	tgggaacaga	togagggcaa	ctocaagctg	1440
aggaocgtgg	gcagcaaoct	gtgocggac	agtogcagcg	ocaagagocg	gggocaaag	1500
gtggaggtgt	gtggococgc	ooccttgcag	cagtggaaagt	tcacgctcaa	oocgcagcag	1560

**FIG. 14B**

SUBSTITUTE SHEET (RULE 26)

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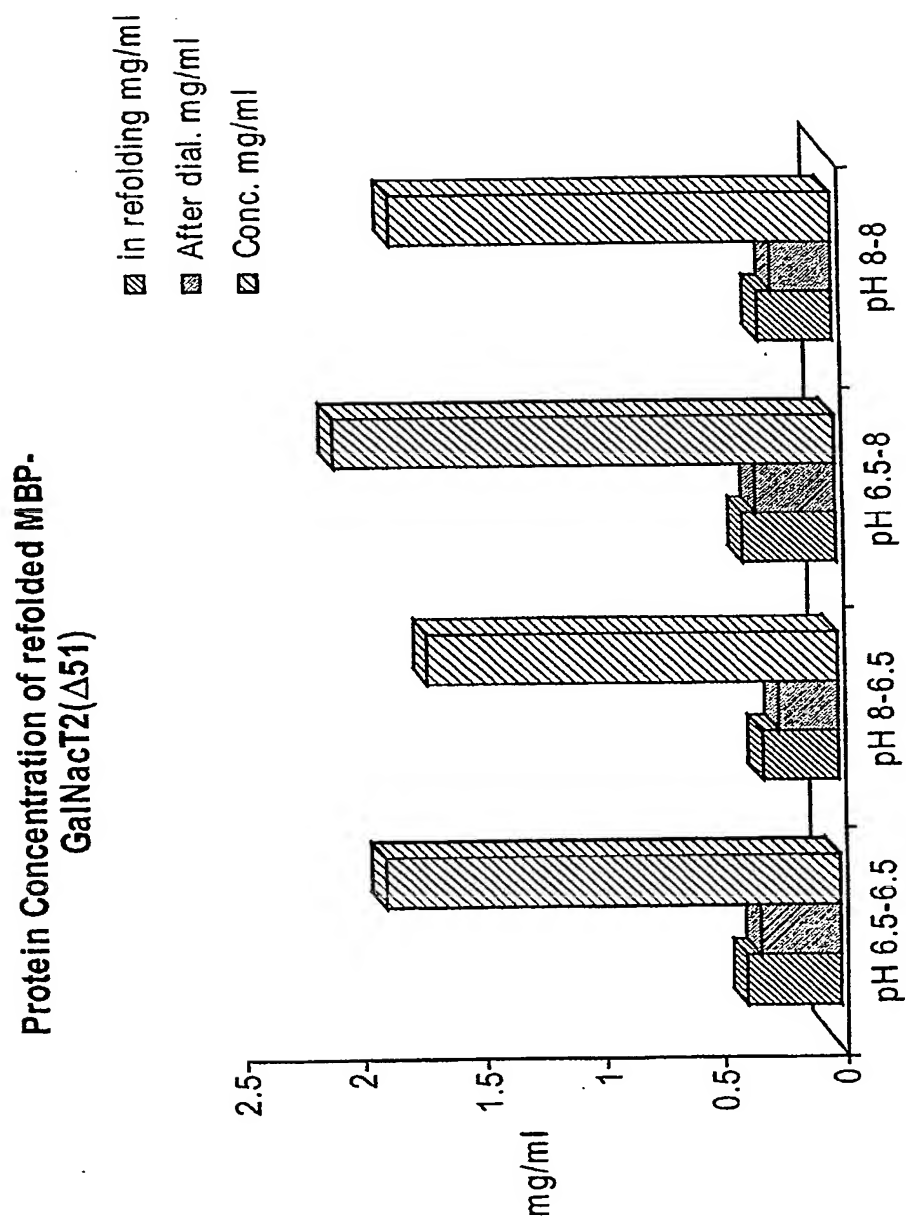
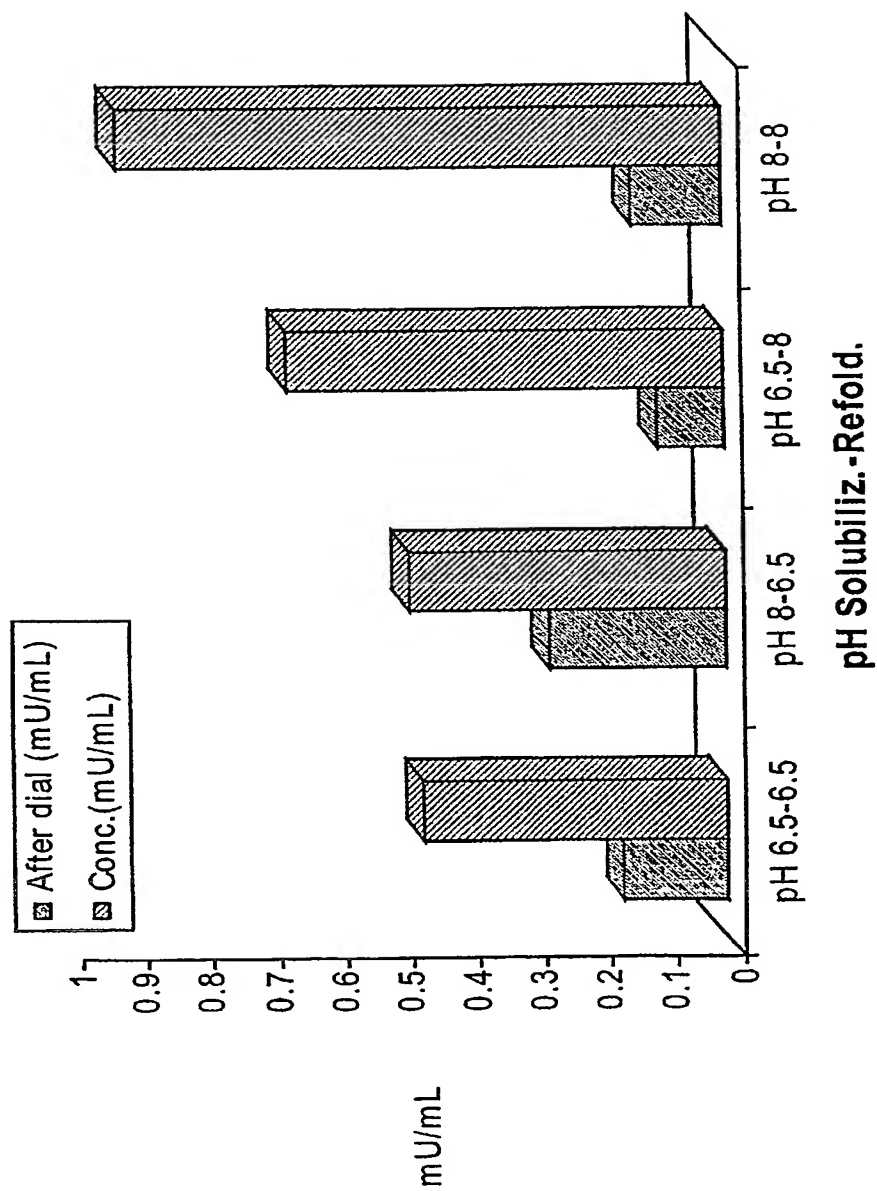


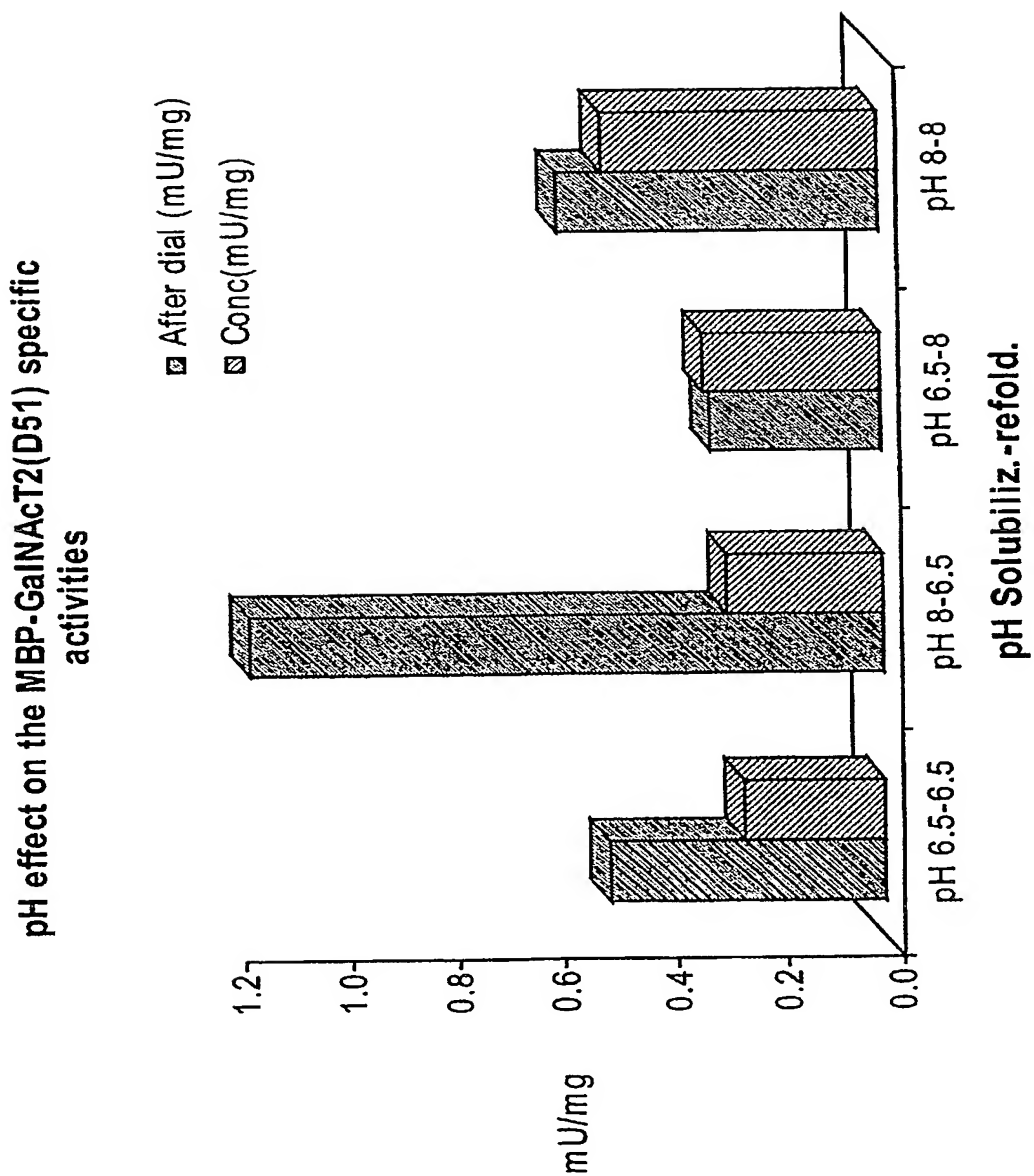
FIG. 15

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GalNAcT2 activities of refolded MBP-  
GalNAcT2(D51)

**FIG. 16**

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**FIG. 17**

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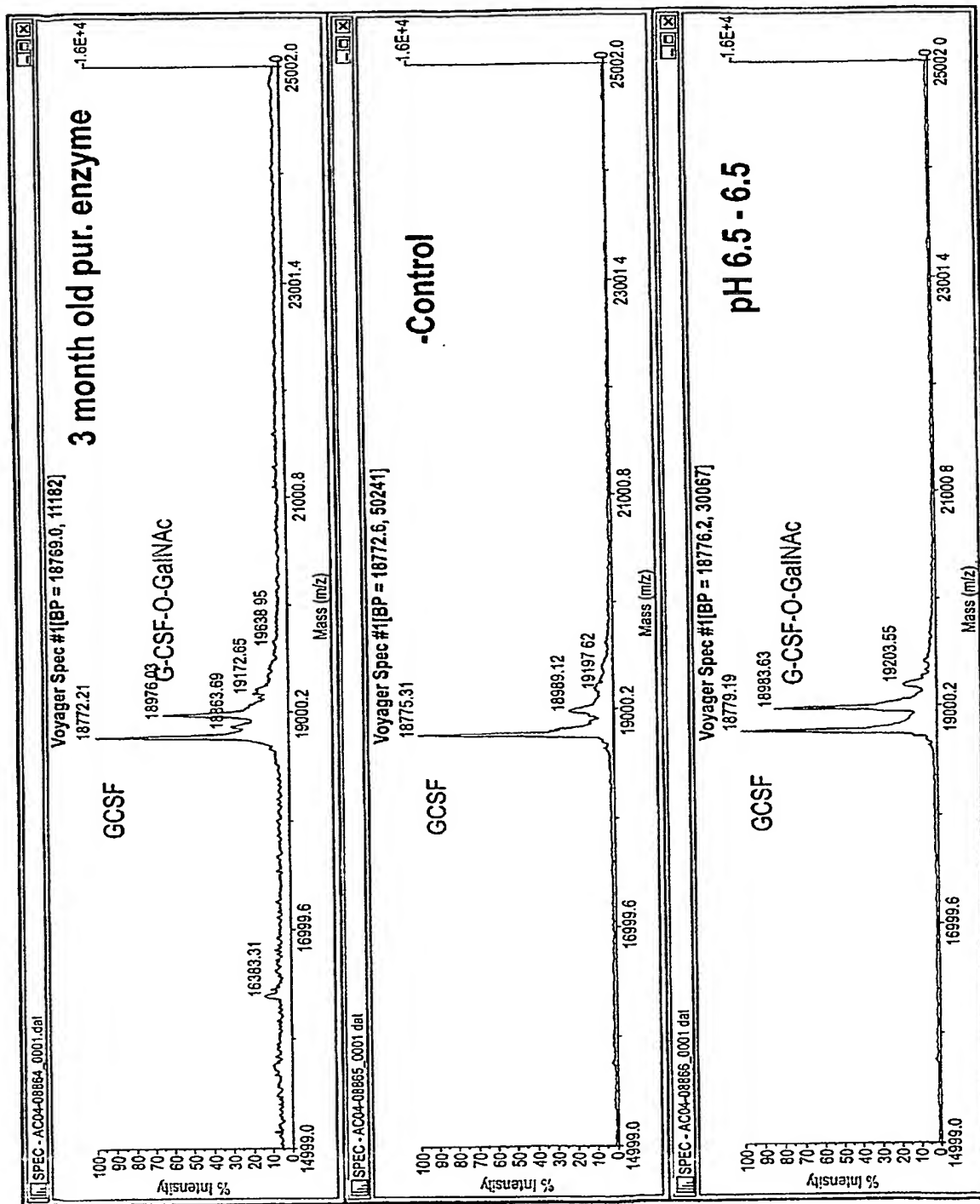


FIG. 18A

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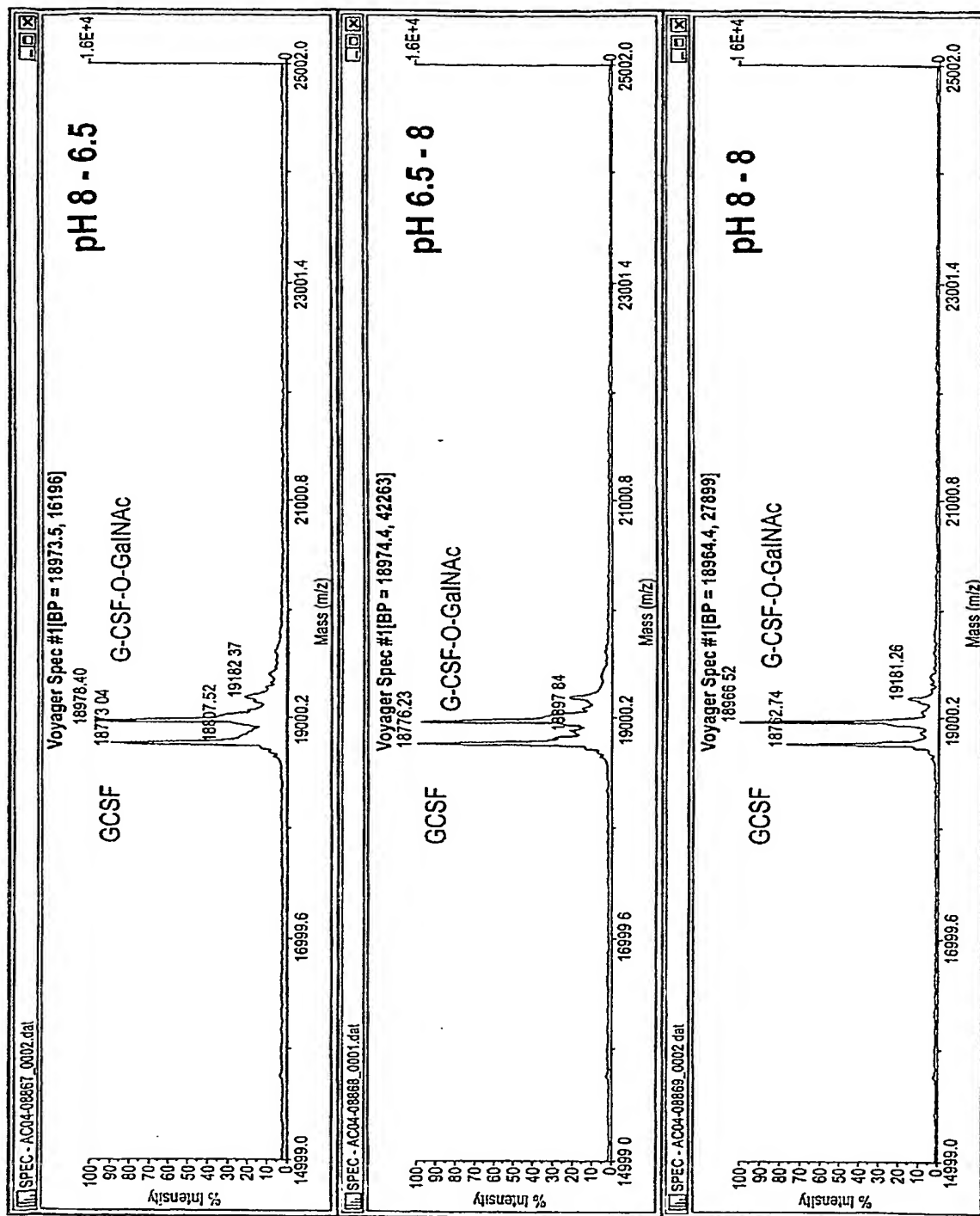


FIG. 18B

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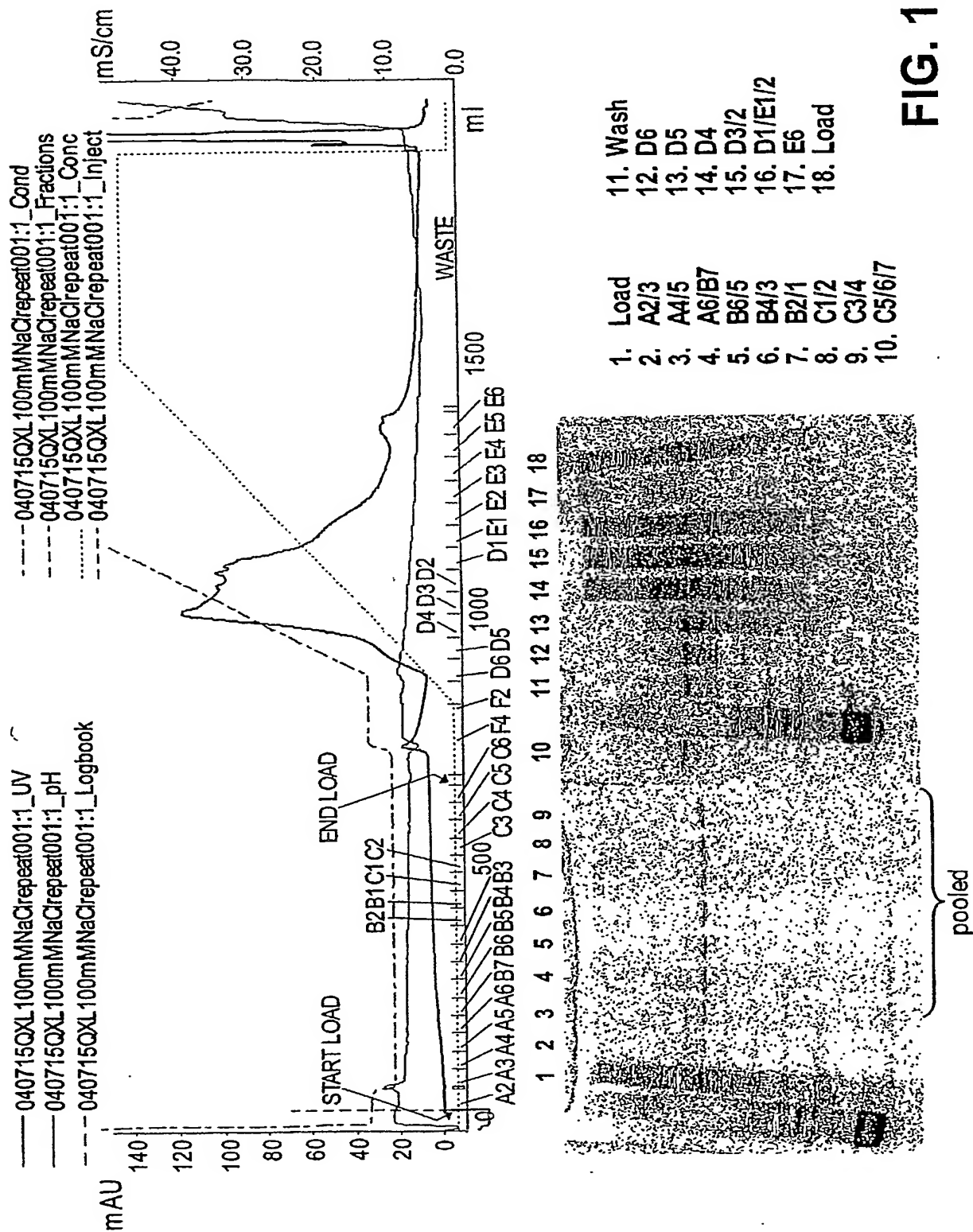


FIG. 19



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	Volume (mL)	Activity (U/L)	A280
Load	890	1.5	0.110
FT <sub>A4-C4</sub>	670	9.2	NA
FT <sub>C5-C7</sub>	120	1.0	0
Wash	138	3.6	0.100
D6	45	4.5	0
D5	45	2.4	0.026
D4	45	2.0	0.108
D3/2	90	1.1	0.179
E6		0.0	0.017

**FIG. 20**

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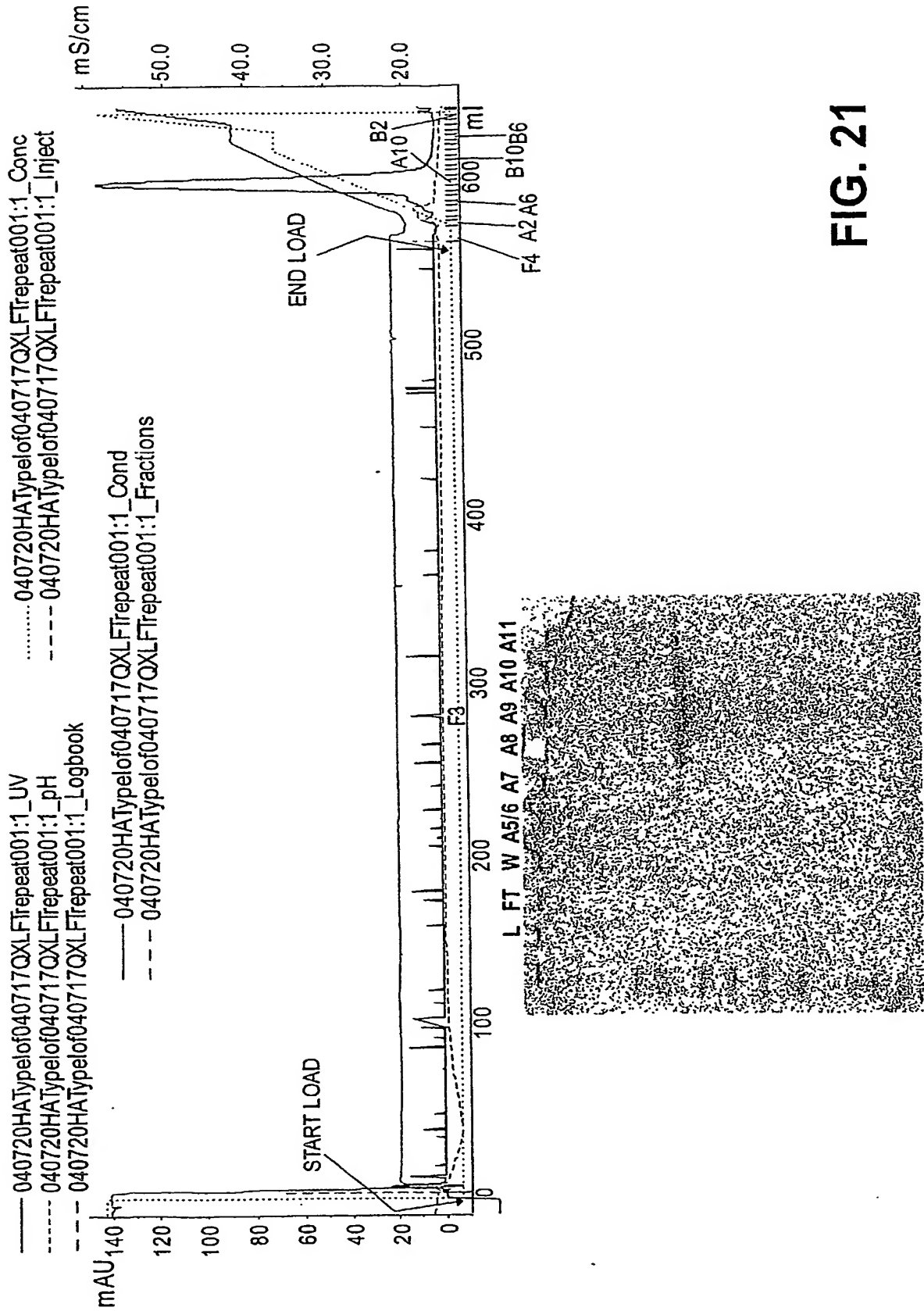


FIG. 21

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Pooled A4-C4 and adjusted pH to 7.0 using 1mM HCl 670mL  
load pH 7.0 16mS/cm

	Volume (mL)	Activity (U/L) pre- dialysis	Activity (U/L) post- dialysis	A280	A280/ 1.51 (mg/mL)	Activity (U)	Mass (mg)	Specific Activity (U/mg)
Load	670	9.2	NA	NA				
FT	670	0.0	NA	0.122				
Wash	9	2.9	NA	-0.013				
A5/6	6	1.1	NA	-0.005				
A7	3	0.1	19.3 (13mL)	0.180	0.119	0.25	1.55	0.16
A8	3	1.3						
A9	3	4.6						
A10	3	2.4						
A11	3	0.4						

FIG. 22

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COMPARISON of MBP with MBP-SBD<sub>39</sub> tag in ST3Gal3 in Cyclodextrin column purification

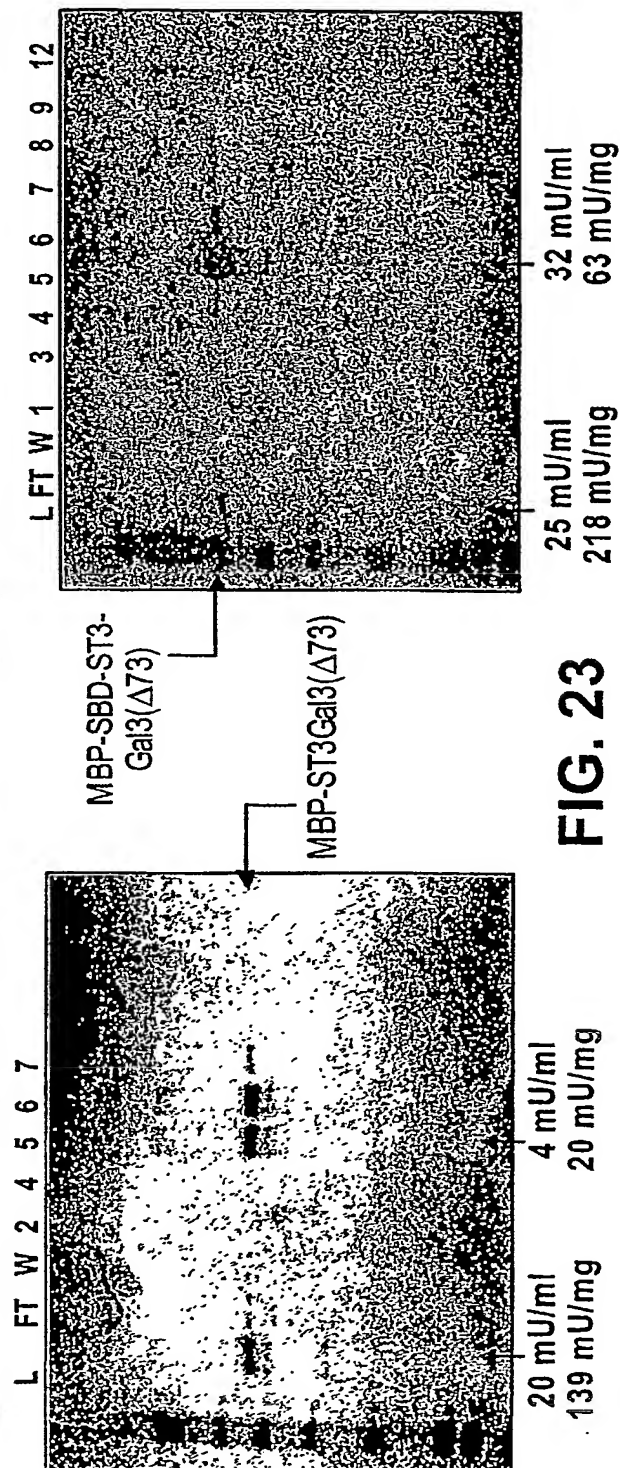
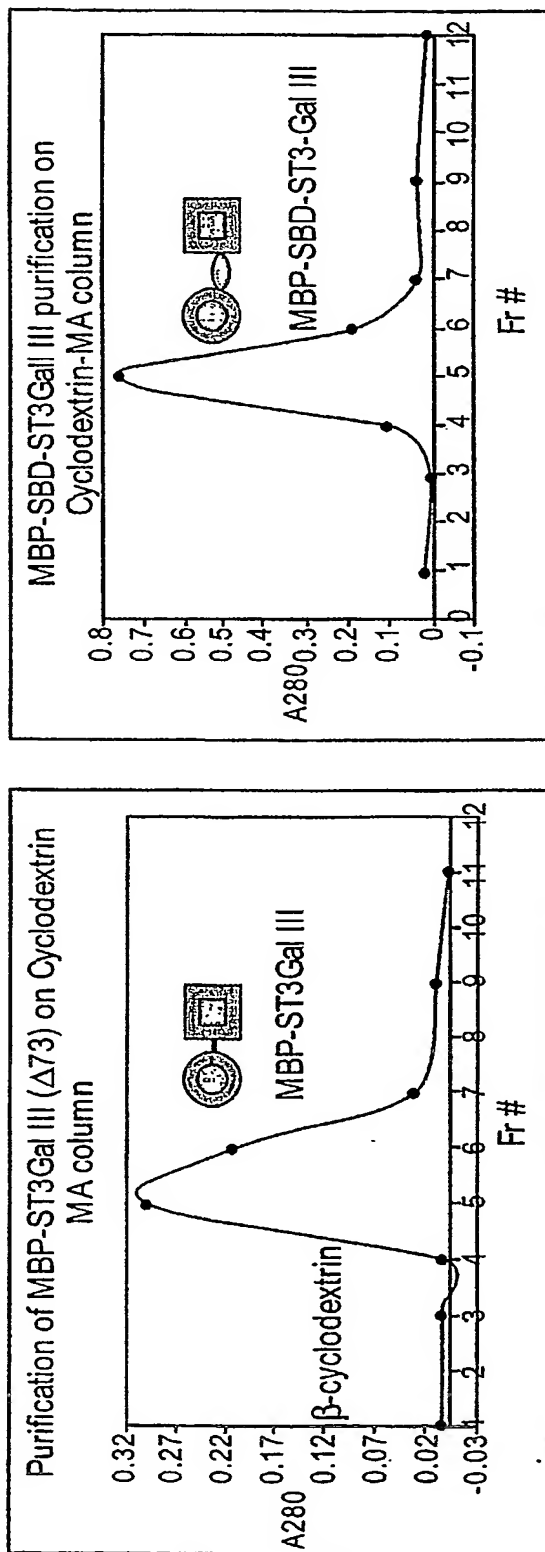


FIG. 23

MBP-pST3Gal1 fusion protein

MKIEEGKLVWINGDKGYNGLAEVGKKFEKDTGIKVTVEHPDKLEEKFPQVAATGDGPDIFWAHDRF  
GGYAQSGLLAEITPDKAFQDKLYPFTWDVRYNGKLIAYPIAVEALSILYNKDLLPNPPKTWEEIPALD  
KELKAKGKSALMFNLQEPYFTWPLIAADGGYAFKYENGYDIKDVGVNDAGAKAGLTFVLDLKNKH  
MNADTDYSIAEAAFNKGETAMTINGPWAWSNIDTSKVNYGVTVLPTFKGQPSKPFVGVLSAGINAASP  
NKELAKEFLENYLLTDEGLEAVNKDKPLGAVALKSYEEELAKDPRIAATMENAQKGEIMPNIPQMSAF  
WYAVRTAVINAASGRQTVDEALKDAQTNSSNNNNNNNNNLGIEGRISEFGSELSENFKKLKMKYPYR  
PCTCTRCIEEQRVSAWFDERFNRSMQPLLTAKNAHLEEDTYKWWLRLQREKQPNNLNDTREL FQVVP  
GNVDPLLEKRLVSCRRCVVGNSGNLKESYYGPQIDSHDFVLRMNKAPTEGFEADVGSKTTHHFVYPE  
SFRELAQEVSMILVPFKTTDLEWVISATTTGRISHTYVPVPAKIKVKEKILYHPAFIKYVFDRLQGH  
GRYPSTGILSVFSLHICDEVLDLYGFGADSKGNWHHYWENNPSAGAFRKTGVHDGDFESNVTTLASIN  
KIRIFKGR

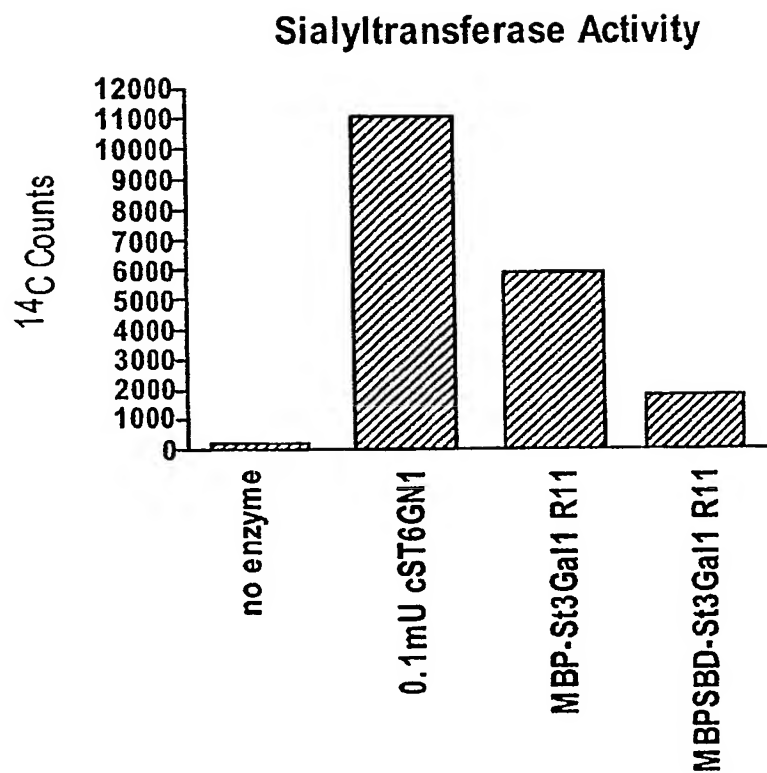
FIG. 24A

MBPSBD-pST3Gal1 fusion protein

MKIEEGKLVWINGDKGYNGLAEVGKKFEKDTGIKVTVEHPDKLEEKFPQVAATGDGPDIFWAHDRF  
GGYAQSGLLAEITPDKAFQDKLYPFTWDVRYNGKLIAYPIAVEALSILYNKDLLPNPPKTWEEIPALD  
KELKAKGKSALMFNLQEPYFTWPLIAADGGYAFKYENGYDIKDVGVNDAGAKAGLTFVLDLKNKH  
MNADTDYSIAEAAFNKGETAMTINGPWAWSNIDTSKVNYGVTVLPTFKGQPSKPFVGVLSAGINAASP  
NKELAKEFLENYLLTDEGLEAVNKDKPLGAVALKSYEEELAKDPRIAATMENAQKGEIMPNIPQMSAF  
WYAVRTAVINAASGRQTVDEALKDAQTNSSNNNNNNNNNLGIEGRISEFGSIVATGGTTTATPTG  
SGSVTSTSKTTATASKTSTSTSTCTPTTAVAVTFDLTATTTYGNIYLVGSISQLGDWETSDGIALSAD  
KYTSSDPLWYVTVTLPAGESEYKFIRESDDSVWESDPNREYTVPQACGTSTATVTDTWRGSELSEN  
FKKLKMKYPYRPTCTRCIEEQRVSAWFDERFNRSMQPLLTAKNAHLEEDTYKWWLRLQREKQPNNLN  
DTIRELFQVVPGNVDPLLEKRLVSCRRCVVGNSGNLKESYYGPQIDSHDFVLRMNKAPTEGFEADV  
SKTTHHFVYPESFRELAQEVSMILVPFKTTDLEWVISATTTGRISHTYVPVPAKIKVKEKILYHPAFIK  
YVFDRLQGHGRYPSTGILSVFSLHICDEVLDLYGFGADSKGNWHHYWENNPSAGAFRKTGVHDGDF  
ESNVTTLASINKIRIFKGR

FIG. 24B

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Test pST3Gal1 for activity after Hampton refold

**FIG. 25**

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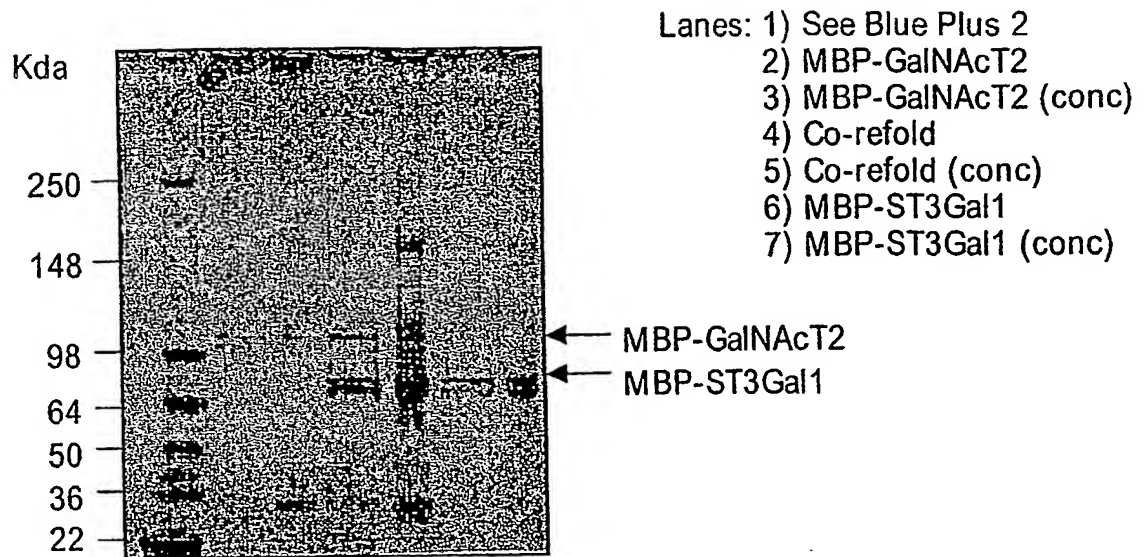
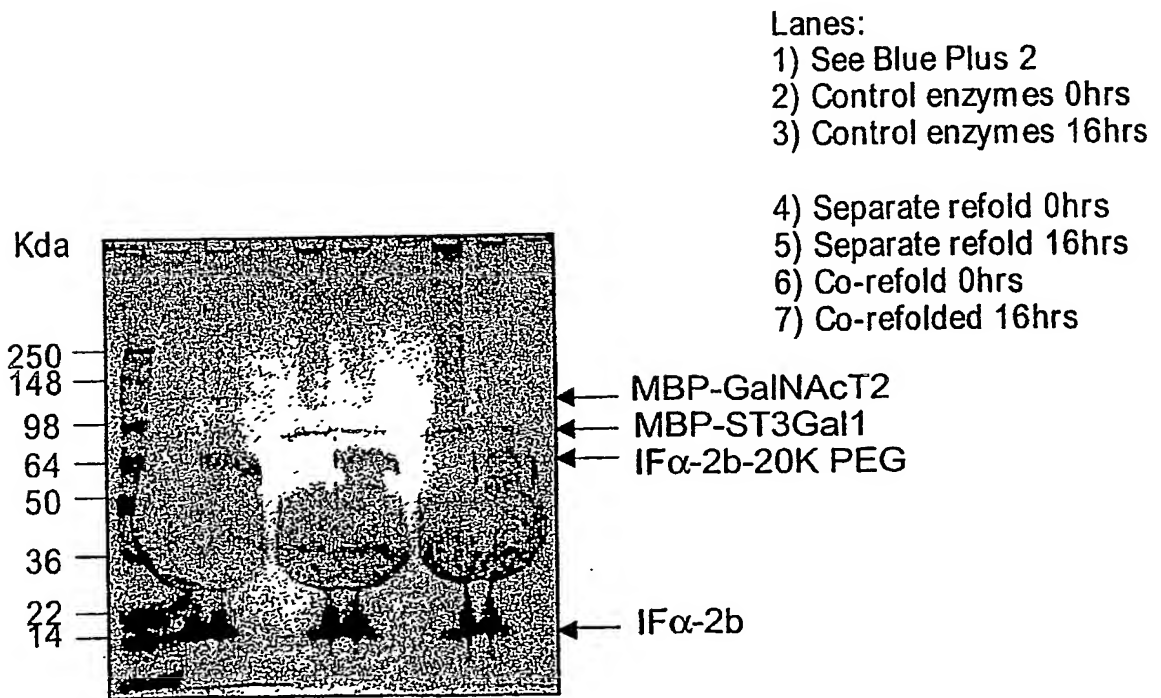
MKIEGKLVWINGDKGYNGLAEVGKKFEKDTGKVTVEHPDKLEKFPQVAATGDGPDIFWAHDRF  
 GGYAQSGLLAEITPDKAFQDKLYPFTWDVRYNGKLIAYPIAVEALSLIYNKDLLPNPPKTWEEIPALD  
 KELKAKGKSALMFNLQEPYFTWPLIAADGGYAFKYENGYDIKDVGVDNAGAKAGLTFLVDLIKNGH  
 MNADTDYSIAEAAFNKGETAMTINGPWAWSNIDTSKVN YGTVLPFTFKGQSPKPFVGVLSAGINAASP  
 NKElakefLENYLLTDEGLEAVNKDKPLGAVALKSYEEELAKDPRIAATMENAOQGEIMPNIPQMSAF  
 WYAVRTAVINAASGRQTVDEALKDAQTNSSNNNNNNNNNNNLGIEGRSEFGSSEHLDDKVPRTPGAL  
 STRKTPMATGAVPAKKKVQATKSPASSPHPTTRRRQRLKASEFKSEPRWDFFEEYSLDMSSLQT  
 NCSASV KIKASKSPWLQNIPLPNTILFSDSGRFTQSEWNRLEHFAPPFGFEMELNQSLVQKVVTFRP  
 PVRQQQLLASLPTGYSKCITCAVVGNGGILNDSRVGREIDSHDYVFRLSGAVIKGYEQDVGTRT  
 SFYGFTAFSLTQSILILGRRGFQHVPLGKDVRYLHFELEGTRNYEWLEAMFLNQTLAKTHLSWFR  
 HRPQEAFRNALDLDRYLLHPDFLRMYMKNRFLRSKTLDTAXWRIYRPTTGALLLTALHLCDKV  
 SAYGFITEGHERFSDDHYDTSWKRLIFYNHDFFRLERMVWKRLHDEGIWLYQRPQSDKAKN

FIG. 26A

MKIEGKLVWINGDKGYNGLAEVGKKFEKDTGKVTVEHPDKLEKFPQVAATGDGPDIFWAHDRF  
 GGYAQSGLLAEITPDKAFQDKLYPFTWDVRYNGKLIAYPIAVEALSLIYNKDLLPNPPKTWEEIPALD  
 KELKAKGKSALMFNLQEPYFTWPLIAADGGYAFKYENGYDIKDVGVDNAGAKAGLTFLVDLIKNGH  
 MNADTDYSIAEAAFNKGETAMTINGPWAWSNIDTSKVN YGTVLPFTFKGQSPKPFVGVLSAGINAASP  
 NKElakefLENYLLTDEGLEAVNKDKPLGAVALKSYEEELAKDPRIAATMENAOQGEIMPNIPQMSAF  
 WYAVRTAVINAASGRQTVDEALKDAQTNSSNNNNNNNNNNNLGIEGRSEFGSSEHLDDKVPRTPGAL  
 NIKERSLQSLAKPKSQAPTRARRITIVAEPYPENNALNTQTQPKAHTTGDRGKEANQAPPEEQDK  
 VPHTAQRAAAWKSPEKEKTMVNTLSPRGQDAGMASGRTEAQSWSQSDTKTTQCGNGGQTRKLTIA  
 SRTVSEKHQKAAATTAKTLIPKSQHRMLAPTGA VSTRKQKGVTTAVPPKEKPKQATPPAPFQ  
 SPTTQRNQRKKAANFKSEPRWDFFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLFPLNLTFLDS  
 RHFNQSEWDRLEHFAPPFGFEMELNYSLVQKVVTFRPPVQQLLASLPA GSLRCITCAVVGNG  
 GILNNSHMGQEIDSHDYVFRLSGALIKGYEQDVGTIKSFYGFIAFSLTQSLILGNRGFKNVPLGK  
 DVRYLHFELEGTRDYEWEALLMNQTVMSKNLFWFRHRPQEA FREALHMDRYLLHPDFLRMY  
 KNRFRLSKTLDG AHWRIYRPTTGALLLTALQLCDQVSAYGFITEGHERFSDDHYDTSWKRLIFY  
 INHDFKLEREVWKRLHDEGIWLYQRPQGTAKAKN

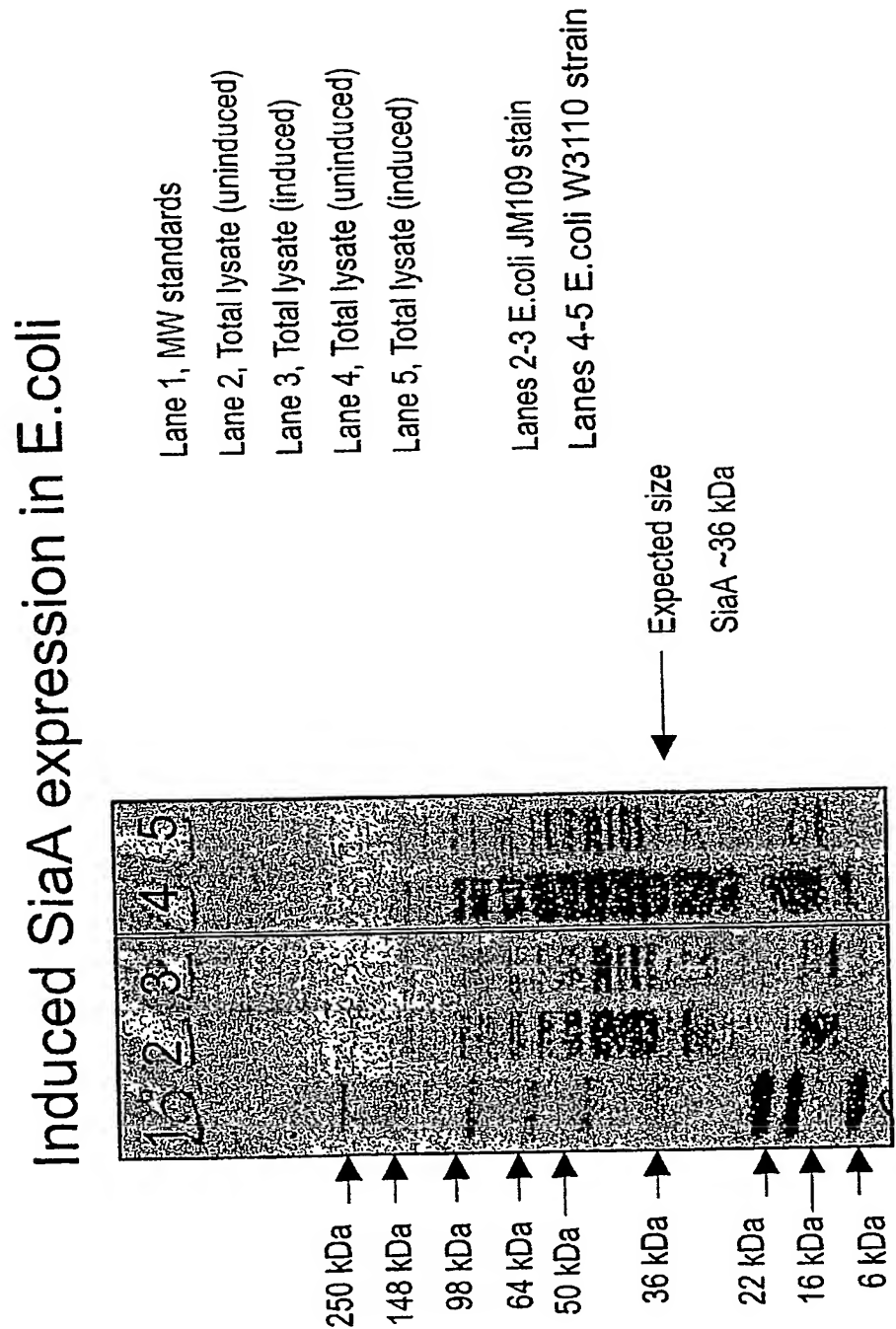
FIG. 26B

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**FIG. 27A****FIG. 27B**



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There is no obvious inducible band at the expected  
Mass of 36 kDa for the native SiaA protein.

FIG. 28

Induced SiaA/MBP expression in E.coli

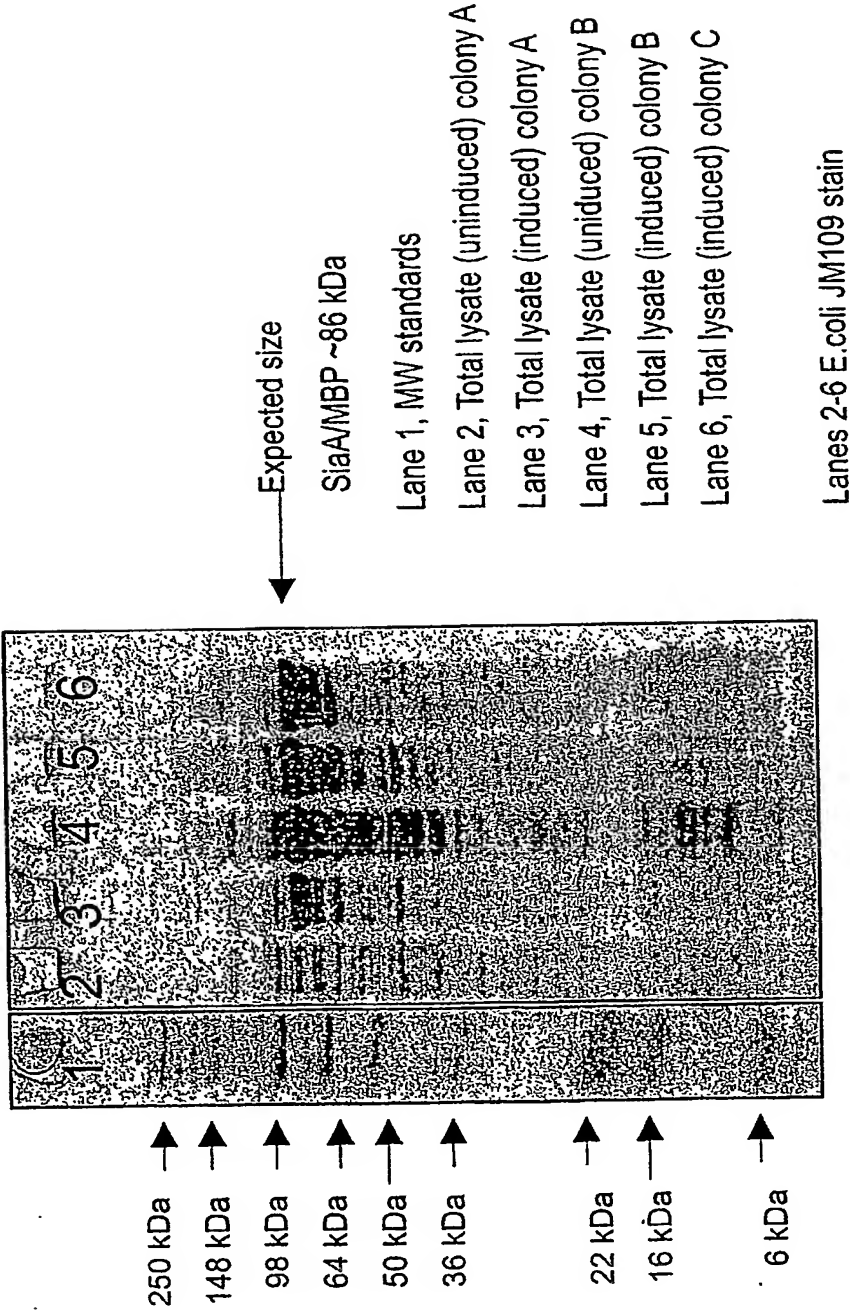


FIG. 29

High level production of SiaA/MBP even in absence of IPTG induction. Compare to figure X where SiaA production is not obvious. The presence of the fusion partner (MBP) drives high levels of expression.

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1 mkfrep1l1gg saampgas1q racr1lvavc alhlgvtlv ylagrd1rrl pqlvgvhppl  
61 qgsshgaaai gqpsgelrlr gvapppp1qn sskprsraps nldayshpgp gpgpgsnlts  
121 apvpstttrs 1tacpeespl lvgpmliefn ipvd1kl1eq qnpkvklggr ytpmdc1sph  
181 kvaii1lfrn rgeh1kywly ylhpmvqrqq ldygiyving agesmfnrak llnvgfkeal  
241 kdydyncfvf sdvd1ipmnd hntyrcfsqp rh1svamd1kf gfs1pyvqyf ggvsa1skqq  
301 flsingfpnn ywgwggeddd iynrlafrgm svsrpnavig kcrmirhsrd knepnpqrf  
361 driahtketm 1sdglnslty mvlevqrypl ytkitvdigt ps

**FIG. 30**

Bovine (b) GalT1 ( $\beta$ 1,4GalT1) constructs

UDP-galactose  $\beta$ -N-acetylglucosaminide  $\beta$ 4-galactosyltransferase (EC 2.4.1.38)

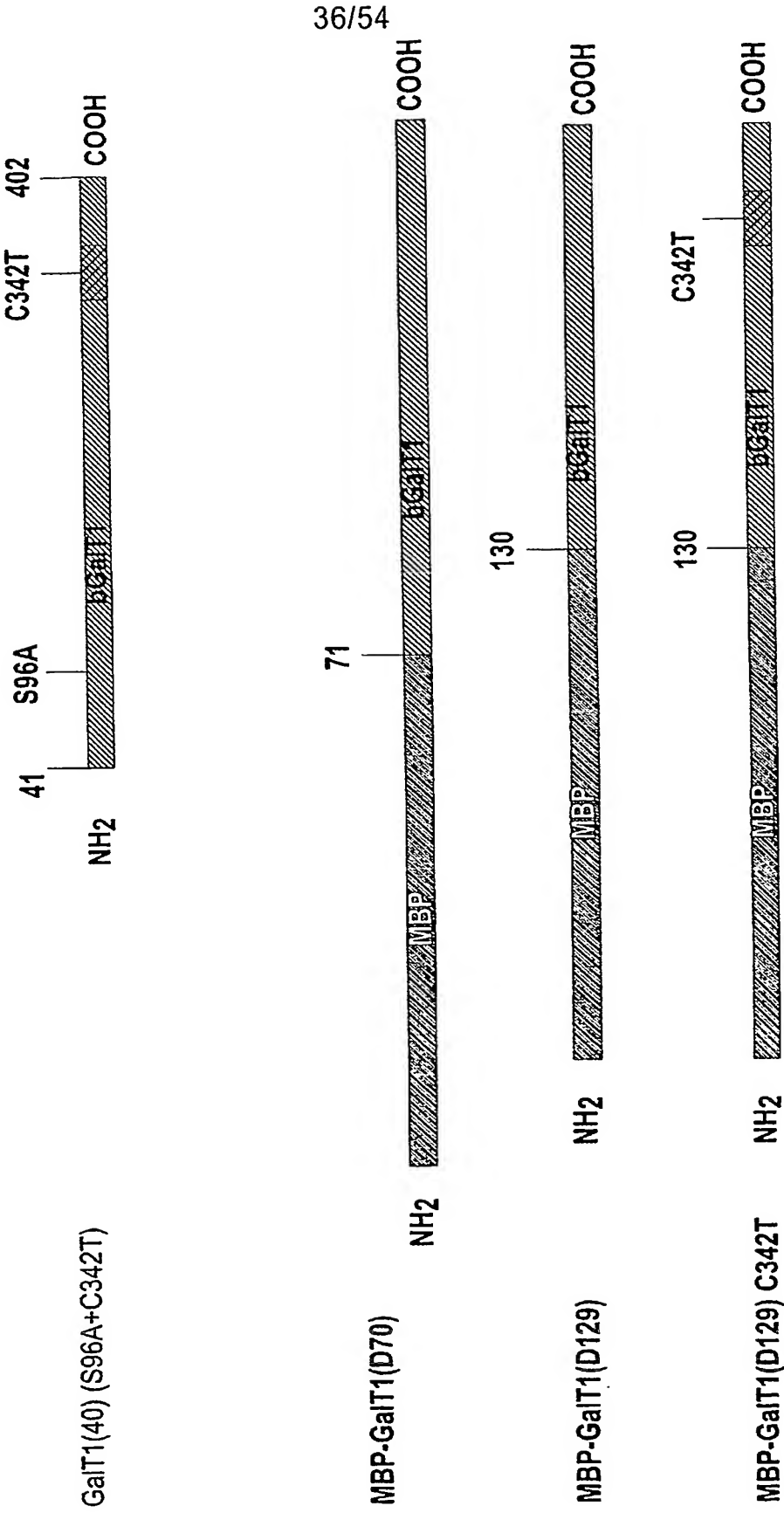
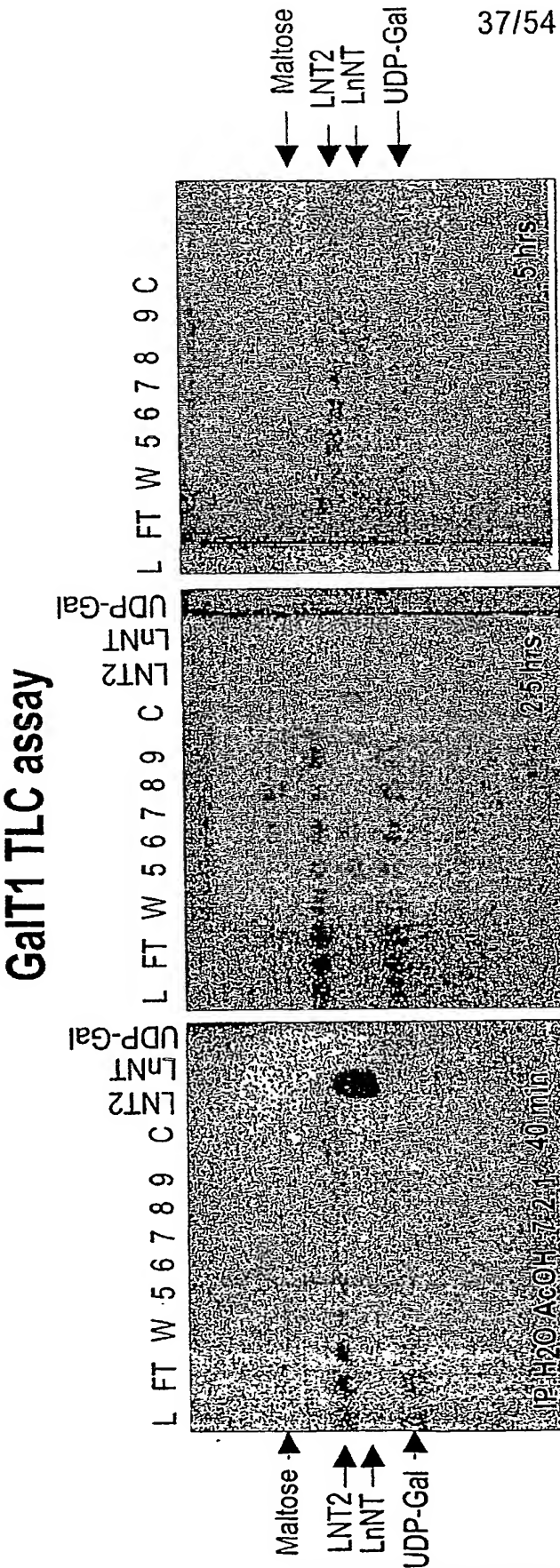


FIG. 31



LnNT reactions with

L: Loaded sample (refolded, dialyzed MBP-GalT1(70) onto amylose column)  
FT: Amylose column Flow trough  
W: Amylose column wash  
5: Maltose Eluted Fr # 5  
6: Maltose Eluted Fr # 6  
7: Maltose Eluted Fr # 7  
8: Maltose Eluted Fr # 8  
9: Maltose Eluted Fr # 9  
C: Control with water

**FIG. 32**

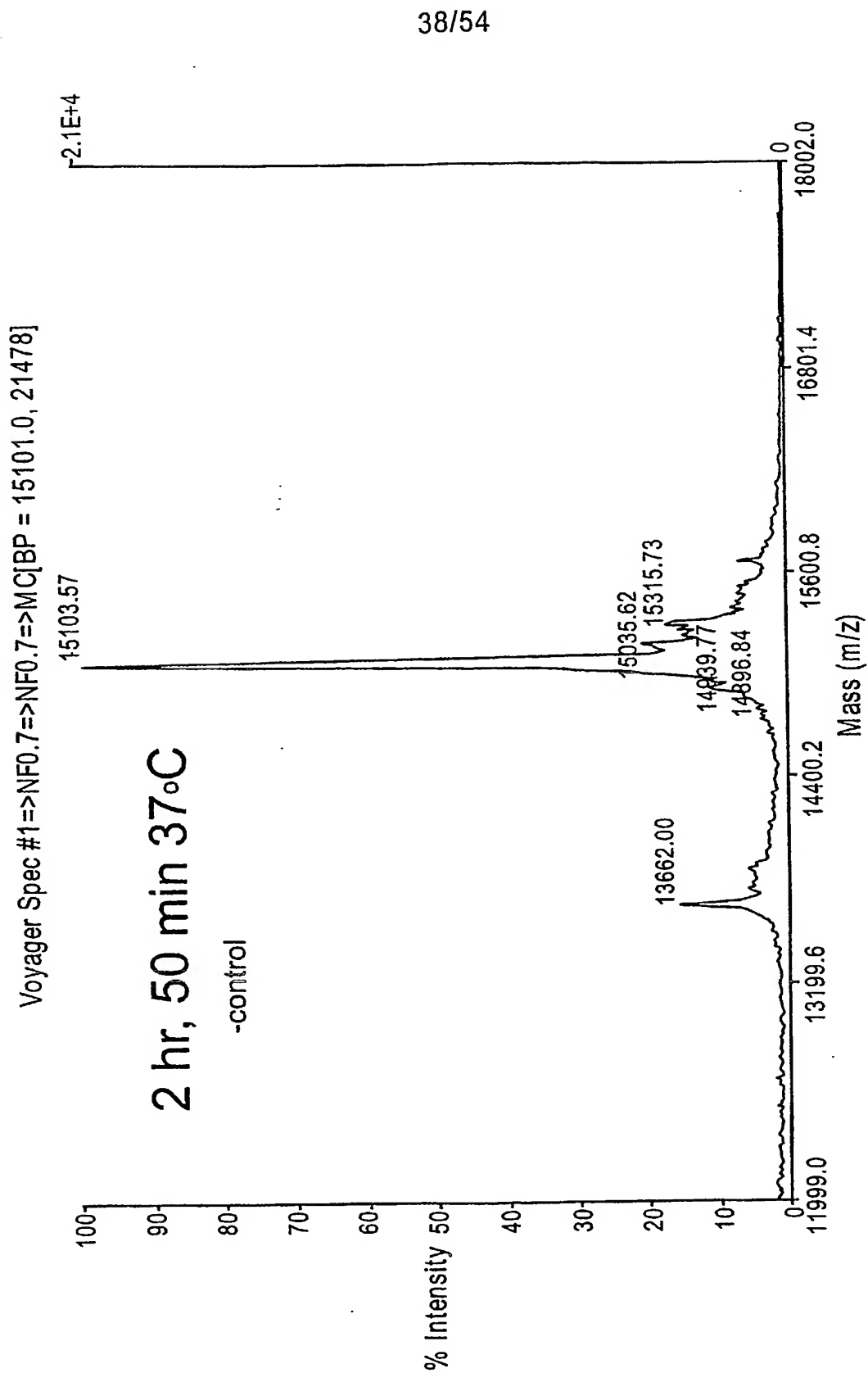


FIG. 33

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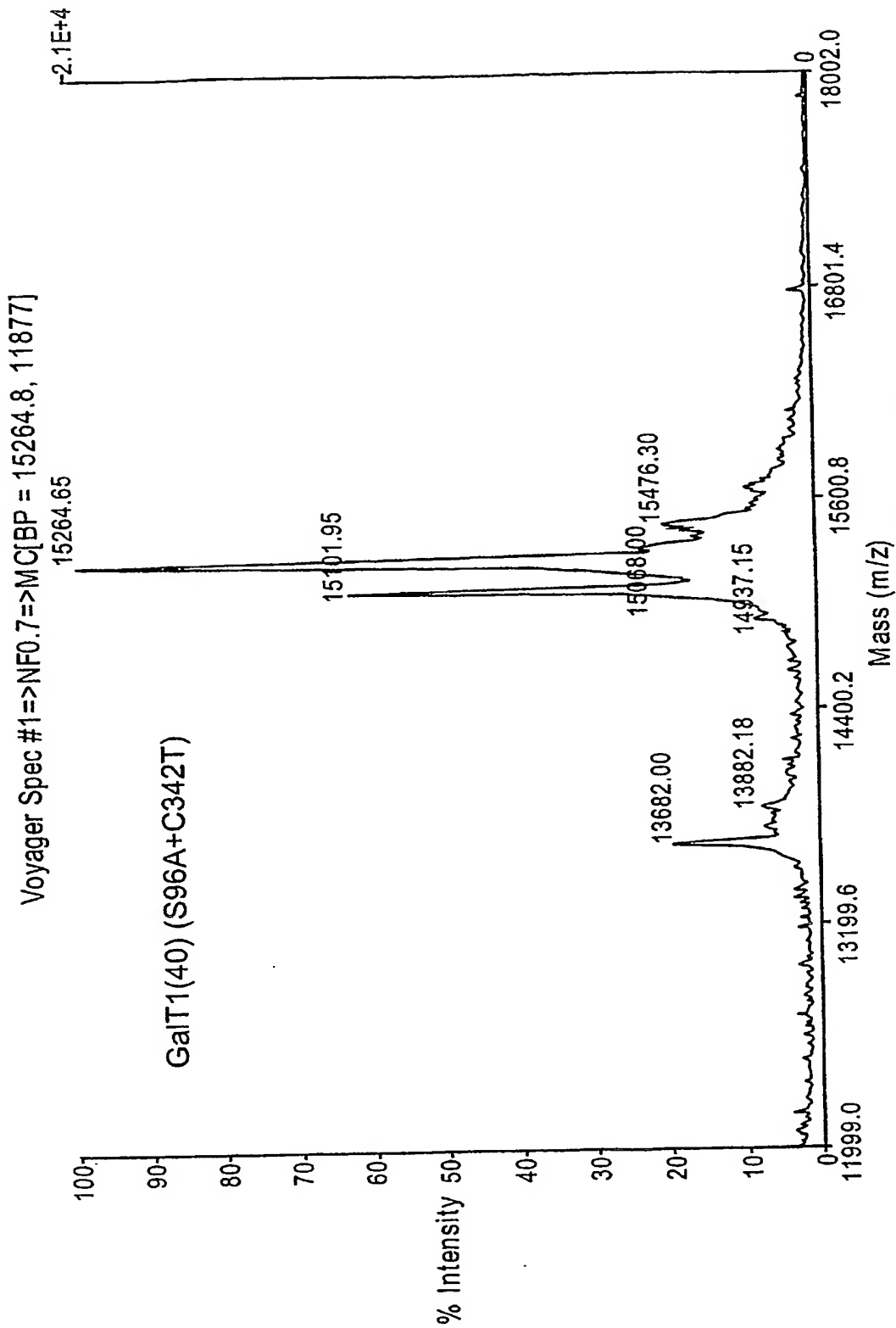
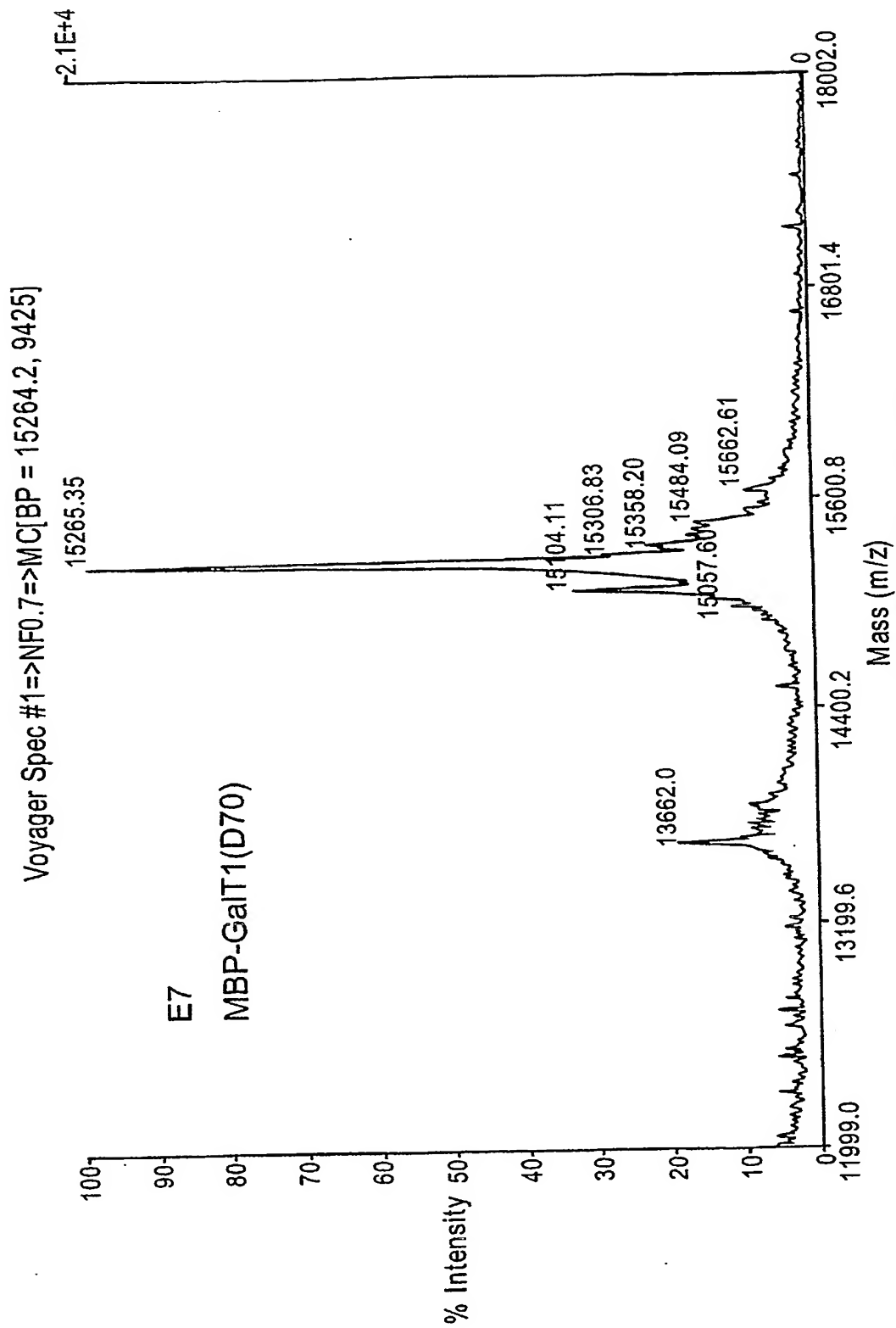


FIG. 33 (CONT.)

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**FIG. 33 (CONT.)**



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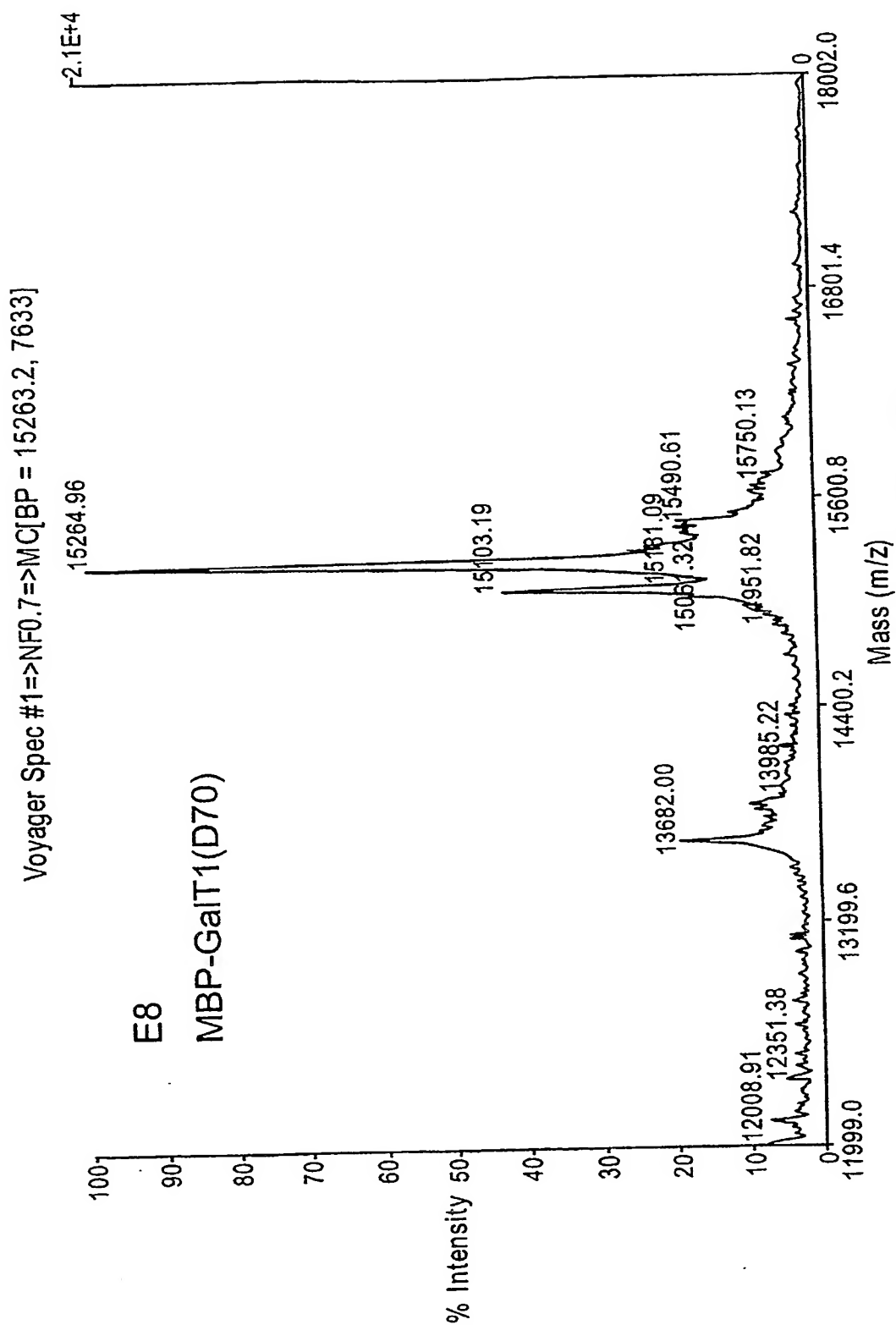


FIG. 33 (CONT.)

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## Kinetics of RNase B modelling with GalT1 6.5.03

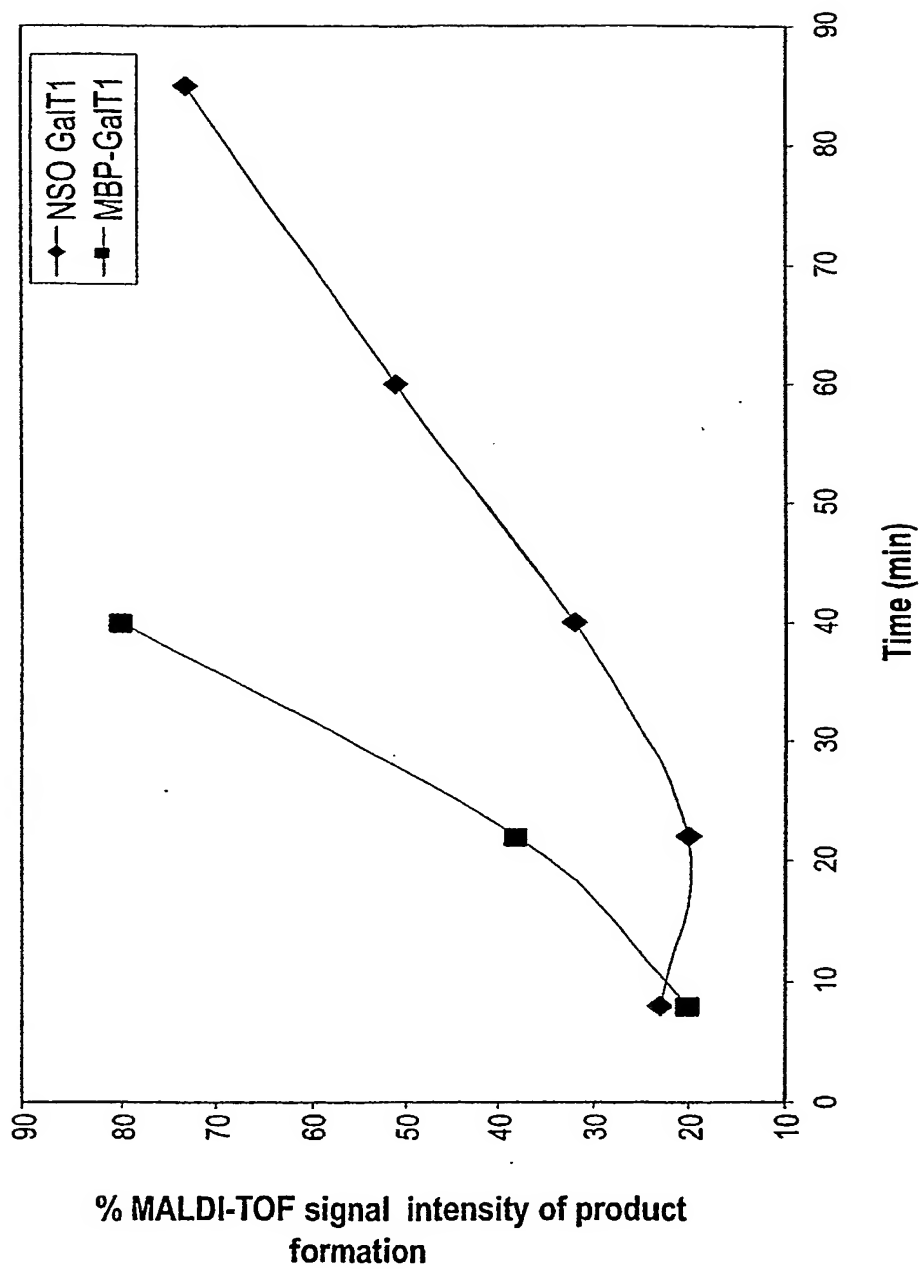
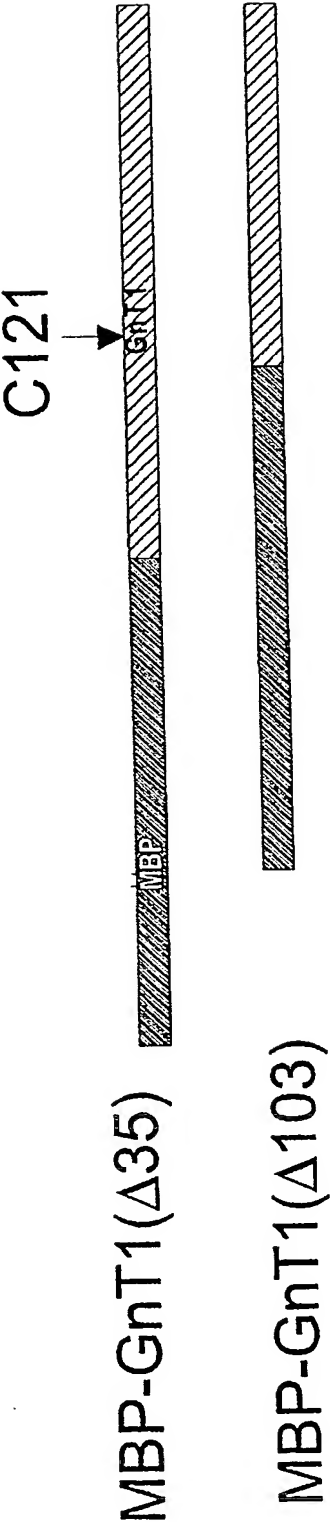


FIG. 34

GnT1 constructs



1 mlkkqsaglv lwgailfvaw nallllffwt rpapgrppsv saldgdpasl trevirlaqd  
61 aevelerqrg llqqigdals sqrgrvptaa ppaqprvpvt papavipilv iacdrstvir  
121 clckllhyrp saelfpiivs qdcgheetaq aiasygsavt hirqpdlssi avppdhrkfq  
181 gyykiarhyr walgvvfrqf rfpaavvved dlevapdffe yfratypllk adpslwcvs  
241 wndngkeqmv dasrpellyr tdffpplglwll laelwaele pkwpkafwdd wmrrepegrqg  
301 racirpeisr tmtfgrkgvs hgqffdqhlk fiklngqfvh ftqldlsylq reaydrdfla  
361 rvygapqlqv ekvrtndrke lgevrvqytg rdsfkafaka lgvmdldksg vpragyrgiv  
421 tfqfrgrrvh lappptwegy dpswn

FIG. 35

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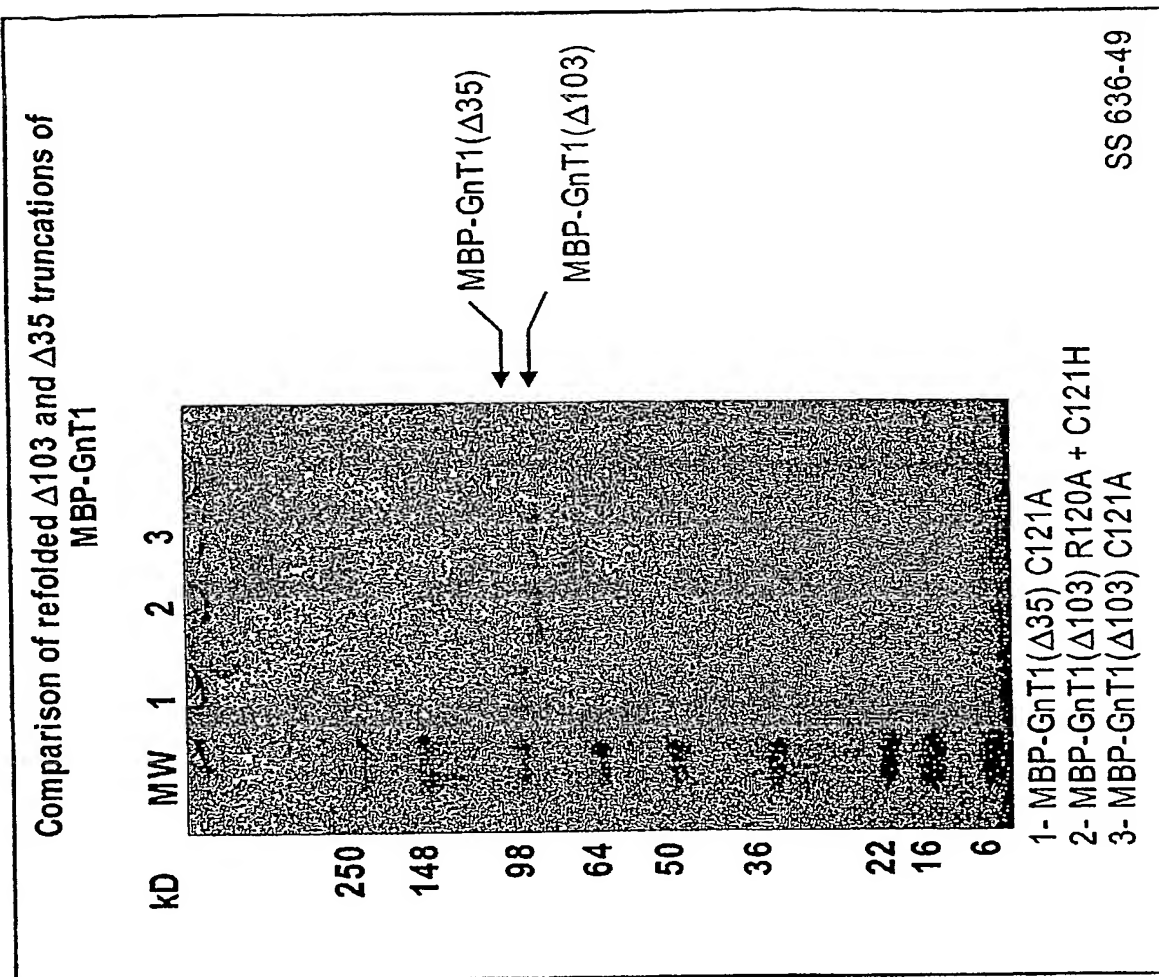
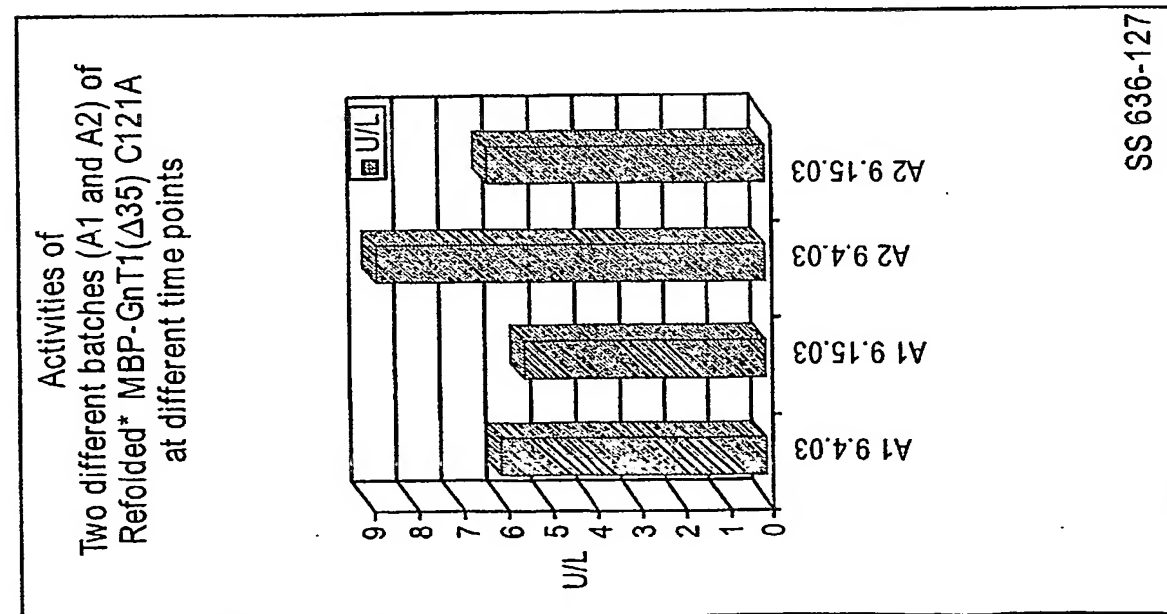


FIG. 36



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1 mapmrkkstl klltllvlfi fltsfflnys htvvttawfp kqmvielesen fkklmkypyr  
61 pctctrciee qrvsawfder fnrsmqpllt aknahleedt ykwwlrlqre kqpnnlndti  
121 relfqvvp gn vdpallekrlv scrrcavvgn sgnlkesyyg pqidshdfvl rmnkaptgef  
181 eadvgsktth hfvy pesfre laqevsmilv pfkttldlewv isatttgtis htyvpvpaki  
241 kvkkekiliiy hpafikyvfd rwlqghgryp stgilsvifs lhicdevdly gfgadskgnw  
301 hhywennpsa gafrktgvhd gdfesnvtti lasinkirif kgr

**FIG. 37**

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## Human ST6GalNAcI

MRSCLRRCRHLSSQGVQWSLLLAVLVFFLFALPSFIKEPQTKPSRHQRTENIKERSLQS  
 LAKPKSQAPTRARRTTIYAEPVPENNALNTQTQPKAHTTGDRGKEANQAPPEEQDK  
 VPHTAQRAAWKSPEKEKTMVNTLSPRGQDAGMASGRTEAQSWKSQDTKTTQNGG  
 GQTRKLTASRTVSEKHQGKAATAKTLIPKSQHRMLAPTGAVSTRTRQKGVTTAVIP  
 PKEKKPQATPPPAPFQSPTTQRNQRLLKAAANFKSEPRWDFEEKYSFEIGGLQTTCPDSV  
 KIKASKSLWLQKLFLPNLTLFLDSRHFNQSEWDRLEHFAPPFGFMELNYSLVQKVVT  
 RFPPVPQQQLLLASLPAGSLRCITCAVVGNNGGILNNSHMGQEIDSHDYVFRLSGALIK  
 GYEQDVGTRTSFYGFTAFSLTQSLLILGNRGFKNVPLGKDVRYLHFLEGTRDYEWLE  
 ALLMNQTVMSKNLFWFRHRPQEAFFREALHMDRYLLLHPDFLRYMKNRFLRSKTL  
 GAHWRIYRPTTGALLLLTALQLCDQVSAYGFITEGHERFS DHYYDTSWKRLIFYINH  
 DFKLEREVWKRLHDEGIIRLYQRP GPGTAKAKN

**FIG. 38A**

## Chicken ST6GalNAcI

MGFLIRRLPKDSRIFRWLLILTVFSFIITSFSALFGMEKSIFRQLKIYQSIHMLQVDTQ  
 DQQGSNYSANGRISKVGLERDIAWLELNTAVSTPSGEGKEEQKKTVKPVAKVEEAK  
 EKVTVKPFPEVMGITNTTASTASVVERTKEKTTARPVPGVGEADGKRTTIALPSMKE  
 DKEKATVKPSFGMKVAHANSTSKDKPKAEPPASVKAIRPVTQAATVTEKKKLRAA  
 DFKTEPQWDFDDEYILDSSSPVSTCSESVRAKAAKSDWLRDLFLPNITLFDKSYFNV  
 SEWDRLEHFAPPYGFMEELNYSLVVEEVM SRLPPNPHQQLLLANSSSNVSTCISCAVVG  
 NGGILNNSGMGQEIDSHDYVFRVSGAVIKGYEKDVGTKTSFYGFTAYSLVSSLQNLG  
 HKGFKKIPQGKHIRYIHFLEAVRDYEWL KALLLDKDIRKGFLNYYGRPRERFDEDF  
 TMNKYLVAHPDFLRYLKNRFLKSKNLQKPYWRLYRPTTGALLLLTALHLCDRVSAY  
 GYITEGHQKYS DHYYDKEWKRLVFYVNHDFNLEKQVWKRLHDENIMKLYQRS

**FIG. 38B**

Mouse ST6GalNAcI protein beginning at residue 32 of the native mouse protein  
 DPRAKDSRCQFIWKNDASAQENQKAEPQVPIMTLSPRVHNKESTSVSSKDLKKQER  
 EAVQGEQAEGKEKRKLETIRPAPENPQSKAEPAAKTPVSEHLDKLPRTPGALSTRKTP  
 MATGAVPAKKKVQATKSPASSPHPTTRRRQRLKASEFKSEPRWDFEEYSLDMSSL  
 QTNCASAVKIKASKSPWLQNIFLPNITLFLDSGRFTQSEWNRLEHFAPPFGFMELNQSL  
 VQKVVTFRPPVRQQQLLLASLPTGYSKCITCAVVGNNGGILNDSRVGREIDSHDYVFR  
 LSGAVIKGYEQDVGTRTSFYGFTAFSLTQSILILGRRGFQHVPLGKDVRYLHFLEGTR  
 NYEWLEAMFLNQTLAKTHLSWFRHRPQEAFFRNALDLDRYLLLHPDFLRYMKNRFL  
 RSKTLDTAHWRIYRPTTGALLLLTALHLC DKVSAYGFITEGHQRFSDHYDTSWKRL  
 IFYINHDFRLERMVWKRLHDEGIWLYQRPQSDKAKN

**FIG. 38C**

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# Hum (h)ST6GalNAcI truncations

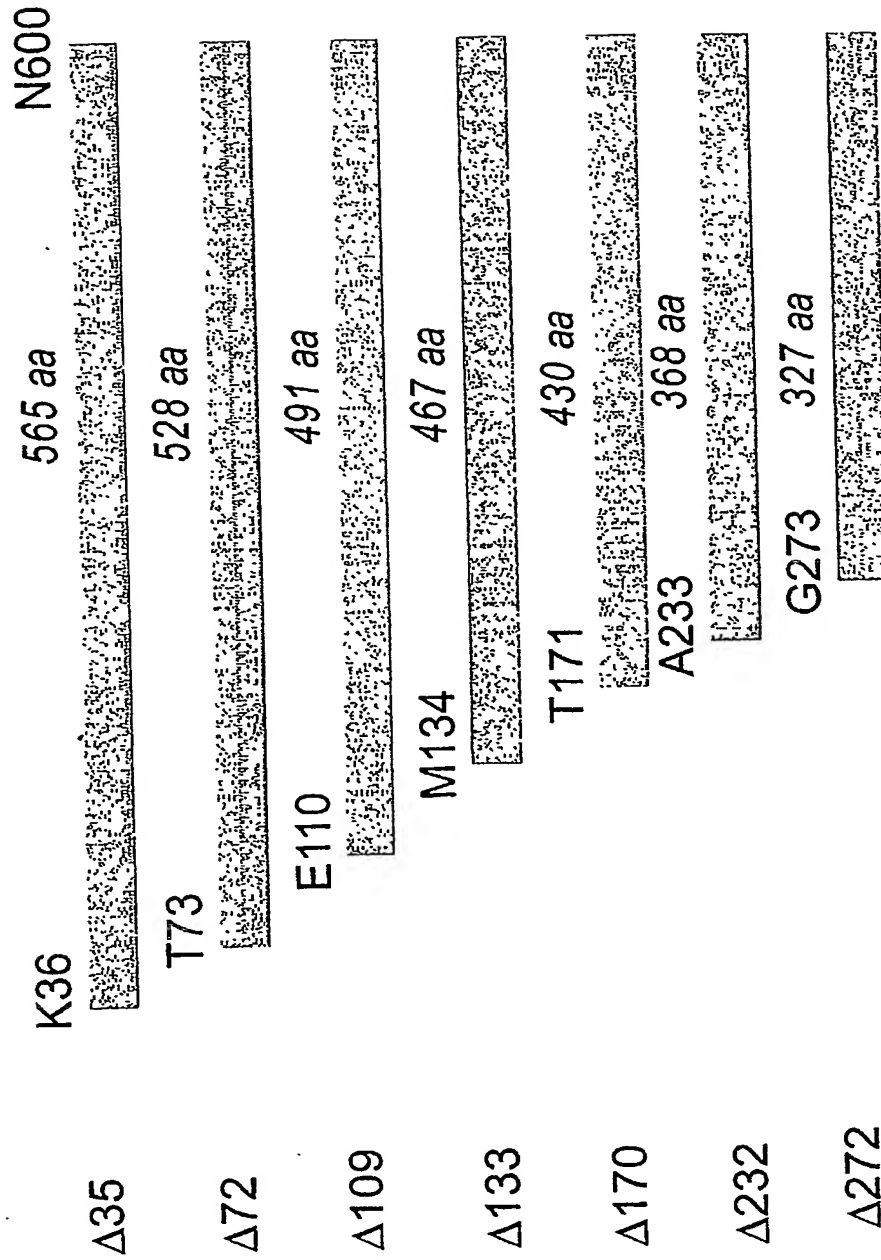


FIG. 39

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# MBP-hST6GalNAc constructs

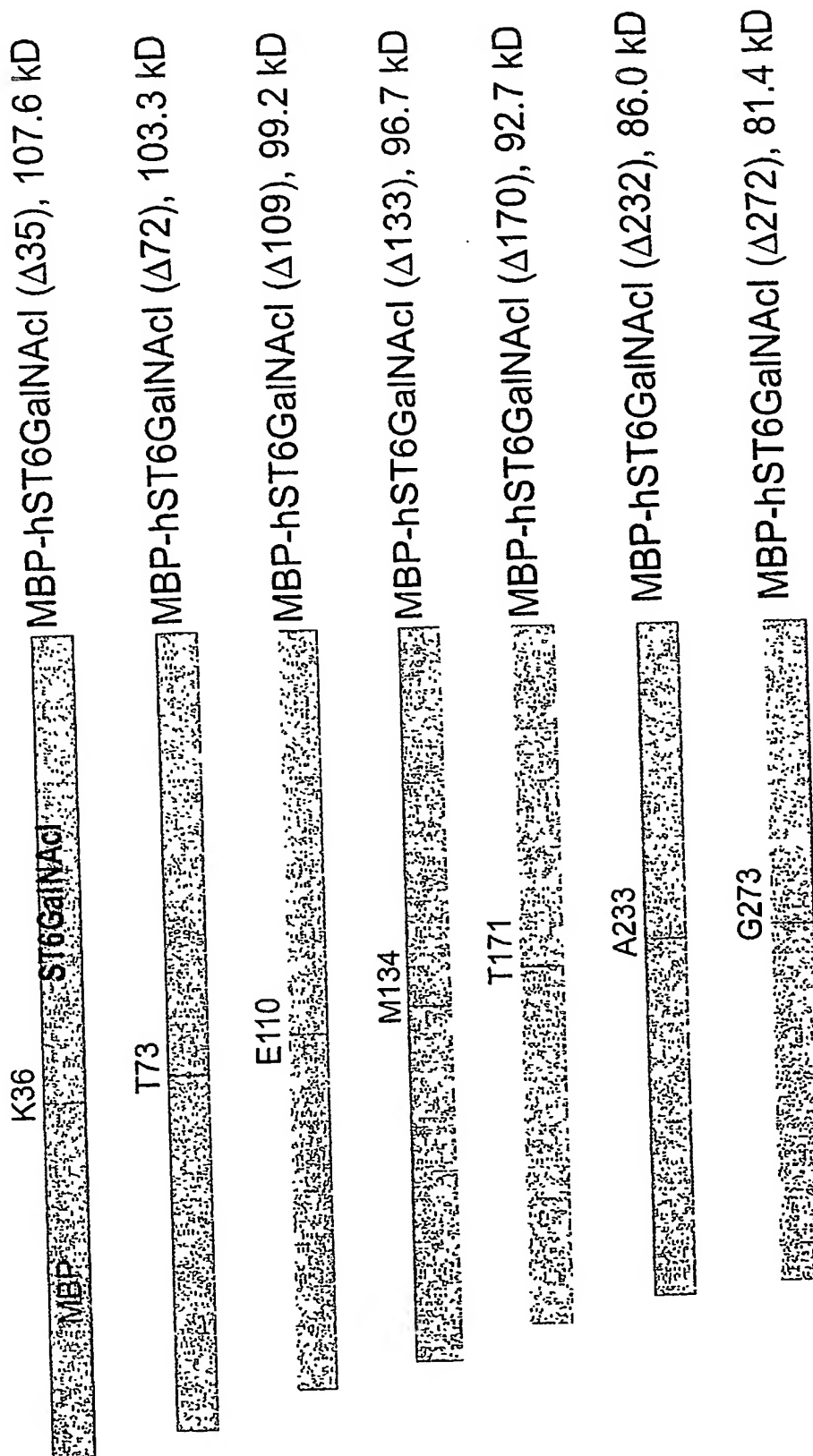


FIG. 40



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MASKSWLNFLTFLCGSAIGFLLCSQLFSILLGEKVDTQPNVLHNDPHARHSDDNGQN  
HLEGQMNFNADSSQHKDENTDIAENLYQKVRILCWVMTGPQNLEKKAKHV KATW  
AQRCNKVLFMSSEENKDFPAVGLKTKEGRDQLYWKTIKAFQYVHEHYLEDADWFL  
KADDDTYVILDNLRWLLSKYDPEEPIYFGRRFKPYVKQGYMSGGAGYVLSKEALKR  
FVDAFKTDKCTHSSSIEDLALGRCMEIMNVEAGDSRDTIGKETFHPPFVPEHHLIKGYL  
PRTFWYWNYNYYPPVEGPGCCSDLAVSFHYVDSTTMYELEYLVYHLRPYGYLYRY  
QPTLPERILKEISQANKNEDTKVKLGNP

**FIG. 41**

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Sequence	Size	Range	Mode		
SC1GALT1.AMI	342	1-	Normal		
SPTS122.AMI	342	1-	Normal		
		10	20	30	40
SC1GALT1.AMI	1	EFMPYDGRH	GDVNDAAHSH	DMEMSGPEQ	DVGGEHVHE
SPTS122.AMI	1	EFMPYDGRH	GDVNDAAHSH	DMEMSGPEQ	DVGGEHVHE
		60	70	80	90
SC1GALT1.AMI	51	EVRVLCWIMT	NPSNHQKKAR	HVKRTWGRKRC	NKLIIFMSSAK
SPTS122.AMI	51	EVRVLCWIMT	NPSNHQKKAR	HVKRTWGRKRC	NKLIIFMSSAK
		110	120	130	140
SC1GALT1.AMI	101	VGEGRNLLWG	KTKEAYKYIY	EHINDADWF	LKADDDTYTI
SPTS122.AMI	101	VGEGRNLLWG	KTKEAYKYIY	EHINDADWF	LKADDDTYTI
		160	170	180	190
SC1GALT1.AMI	151	YSPETPVYFG	CKFKPYVKQG	YMSGGAGYVL	SREAVRRFVV
SPTS122.AMI	151	YSPETPVYFG	CKFKPYVKQG	YMSGGAGYVL	SREAVRRFVV
		210	220	230	240
SC1GALT1.AMI	201	SDNSGAEDVE	IGKCLQNVNV	LAGDSRDSNG	RGRFFFPVPE
SPTS122.AMI	201	SDNSGAEDVE	IGKCLQNVNV	LAGDSRDSNG	RGRFFFPVPE
		260	270	280	290
SC1GALT1.AMI	251	KFWYWOYIFY	KTDEGLDCCS	DNAISFHYVS	PNQMYVLDYL
SPTS122.AMI	251	KFWYWOYIFY	KTDEGLDCCS	DNAISFHYVS	PNQMYVLDYL
		310	320	330	340
SC1GALT1.AMI	301	NTPDALPNKL	AVGELMPEIK	EQATESTSDG	VSKRSTETKT
SPTS122.AMI	301	NTPDALPNKL	AVGELMPEIK	EQATESTSDG	VSKRSTETKT
					Q*.....
					Q*.....

FIG. 42

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*Yersinia* MBP

MKIEEGKLV	WINGDKGYNG	LAEVGKKFEK	DTGIKVTIEH	PDKLEEKFPQ
VAATGDGPD	IFWAHDRFGG	YAQSGLLAEL	TPSKAFQEK	FPFTWDVAVR
NGKLIGYPV	VEALSLIYNK	DLVKEAPKTW	EEIPALDKTL	RANGKSAIMW
NLQEPYFTWP	VIAADGGYAF	KFENGVDYDAK	NVGVNNAGAQ	AGLQFIVDLV
KNKHINADTD	YSIAEAAFNK	GETAMTINGP	WAWSNIDKSK	INYGVTLLPT
FHGQPSKPFV	GVLTAGINAA	SPNKELATEF	LENYLITDQG	LAEVNKKDKPL
GAVALKSFEQ	QLAKDPRIAA	TMDNATNGEI	MPNIPQMAAF	WYATRSVAVLN
AITGRQTVEA	ALNDAATRIT	K		

**FIG. 43A***E. coli* MBP

MKIEEGKLV	WINGDKGYNG	LAEVGKKFEK	DTGIKVTVEH	PDKLEEKFPQ
VAATGDGPD	IFWAHDRFGG	YAQSGLLAEL	TPDKAFQDKL	YPFTWDVAVR
NGKLIAYPIA	VEALSLIYNK	DLLPNPPKTW	EEIPALDKEL	KAKGKSALMF
NLQEPYFTWP	LIAADGGYAF	KYENGKYDIK	DVGVDNAGAK	AGLTFLVDLI
KNKHMNADTD	YSIAEAAFNK	GETAMTINGP	WAWSNIDTSK	VNYGVTVLPT
FKGQPSKPFV	GVLSAGINAA	SPNKELAKEF	LENYLLTDEG	LEAVNKKDKPL
GAVALKSYEE	ELAKDPRIAA	TMENAOQKEI	MPNIPQMSAF	WYAVRTAVIN
AASGRQTVDE	ALKDAQTNS			

**FIG. 43B***Pyrococcus furiosus* MBP

MKIEEGKVVI	WHAMQPNELE	VFQSLAE EYM	ALSPEVEIVF	EQKPNLEDAL
KAAIPTGQGP	DLFIWAHDWI	GKFAEAGLLE	PIDEYVTEDL	LNEFAPMAQD
AMQYKGHYYA	LPFAAETVAI	IYNKEMVSEP	PKTFDEMKA	MEKYYPDANE
KYGIAPWPIA	YFISAIQAQF	GGYYFDDKTE	QPGLDKPETI	EGFKFFFTETI
WPYMAPTGDY	NTQQSIFLEG	RAPMMVNGPW	SINDVKKAGI	NFGVVPLPPI
IKDGKEYWPR	PYGGVKLIYF	AAGIKNKDAA	WKFAKWLTT	EESIKTALALE
LGYIPVLTKV	LDDPEIKNDP	VIYGFQAVQ	HAYLMPKSPK	MSAVWGGVDG
AINAILQDPQ	NADIEGILKK	YQQEILNMQ	G	

**FIG. 43C***Thermococcus litoralis* MBP

MKIEEGKIVF	AVGGAPNEIE	YWKGVIAEFE	KKYPGVTVEL	KRQATDTEQR
RLDLVNALRG	KSSDPDVFLM	DVAWLQGQFIA	SGWLEPLDDY	VQKDNVDLSV
FFQSVINLAD	KQGGKLYALP	VYIDAGLLYY	RKDLLEKYGY	SKPPETWQEL
VEMAQKIQSG	ERETNPFWG	FVWQKGQYEG	LVCDFVEYVY	SNGGSLGEFK
DGKWVPTLNK	PENVEALQFM	VDLIHKKYKIS	PPNTYTEMTE	EPVRLMFQQG
NAAFERNWPY	AWGLHNADDS	PVKGKVGVA	LPHPFGHKSA	ATLGGWHIGI
SKYSDNKALA	WEFVKFVESY	SVQKGFAMNL	GWNPGRVDVY	DDPAVVSKSP
HLKELRAVFE	NAVPRPIVY	YPQLSEIIQK	YVNSALAGKI	SPQEALDKAQ
KEAEELVKQY	SK			

**FIG. 43D***Thermatoga maritime* MBP

MKIEQTKLTI	WSSEKQVDIL	OKLGEEFKAK	YGIPVEVQYV	DFGSIKSKFL
TAAPQGGQAD	IIVGAHDWVG	ELAVNGLIEP	IPNFSDLKNF	YDTALKAFSY
GGKLYGVPIA	MEAVALIYNK	DYVDSVPKTM	DELIEKAKQI	DEEYGGVEVRG
FIYDVANFYF	SAPFILGYGG	YVFKETPQGL	DVTDIGLANE	GAVKGAKLIK
RMIDEGVLTP	GDNYGTMDSM	FKEGLAAMII	NGLWAIKSYK	DAGINYGVAP
IPELEPGVPA	KPFVGVQGF	INAKSPNKVI	AMEFLT NFIA	RKETMYKIYL
ADPRLPARKD	VLELVKDNPD	VVAFTQSASM	GTPMPNVPEM	APVWSAMGDA
LSIIINGQAS	VEDALKEAVD	KIKAQIEK		

**FIG. 43E**

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*Vibrio cholerae* MBP

MKIEEGQLTI	WINGDKGYNG	LAEVGKKFEA	DTGIKVTVAH	PDALQDKFPQ
TAATGDGPD	IFWAHDFRG	YAEAGLLVEI	KPSAKIQEGI	VDFAWDAVKY
NGKIIGYPIA	VESLSLIYNK	DLVPNPPKSW	EEVAELDAKL	KKEGKSAIMW
NLKEPYFTWP	LMAADGGYAF	KYGVDGYDVK	DAGINNKGVK	DAMNFVKGLV
DKGVISPDMD	YSVSESAFNQ	GNTAMTINGP	WSWGNIEKSG	INYGVTTLPK
FNGQASKPFV	GVLTAGISTA	SPNKDLAVEF	IENYLLTNDG	LRMVNNDKPL
GAVALNSFQR	ELDADARIAA	TMDNAMNGEI	MPNIPQMNAF	WSSAKNAIIN
IVDGRQTVDA	ALADA EKQMT	KP		

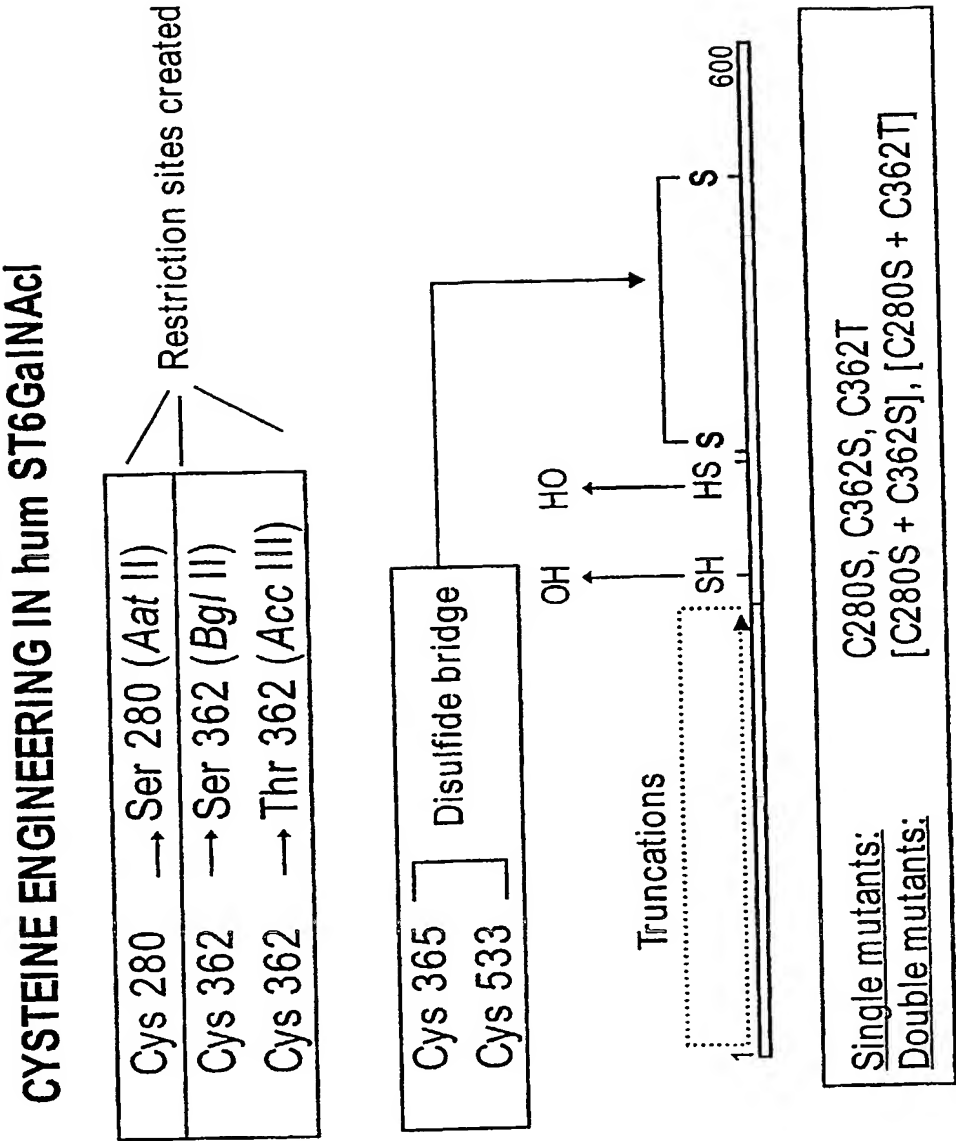
**FIG. 43F**

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	1	50
HSGALNAT1.pep	(1)MRKFAYCKVVLATSLIWVLLDMFLLLYFS-----ECNKC	
HSGALNAT2.pep	(1)MRRRS--RMLLCFAFLWVLGIAYMYSGGGSALAGGAGGGAGRKEDWNEI	
Consensus	(1)MRK A KMLL A IWVL F L D N	
	51	100
HSGALNAT1.pep	(35)DEKKERGLPAGDVLEPVQKPHEGP-G-----EMGKPVVIPKEDQEKMKEM	
HSGALNAT2.pep	(49)DPIKKKDLHHSNGEKAQSMETLPPGKVRWPDFNQEAYVGGTMVRSGQDP	
Consensus	(51)D K K L E Q P G D I D	
	101	150
HSGALNAT1.pep	(79)FKINQFNLMASEMIALNRS L P D V R L E G C K T K V Y P D N L P T T S V V I V F H N E A	
HSGALNAT2.pep	(99)YARNKENQVESDKLRMDRAIPDTRHDQCQRKQWRVDLPATSVVITFHNEA	
Consensus	(101)F N FN M SD I L RAIPD R D C K W LP TSVVI FHNEA	
	151	200
HSGALNAT1.pep	(129)WSTLLRTVHSV IN R S P R H M T E E I V L V D D A S E R D F L K R P L E S Y V K K L K V P V	
HSGALNAT2.pep	(149)RSALLRTVSVLKKSPPHLIKEIILVDDYSN-----DPEDGALLGKIEKV	
Consensus	(151) S LLRTV SVI KSP HLI EIILVDD S P D L V	
	201	250
HSGALNAT1.pep	(179)HVIRMEQRSGLIRARLKGA AVSKGQVITFLDAHCECTV GWLEPLLARIKH	
HSGALNAT2.pep	(194)RVL R N D R R E G L M R S R V R G A D A A Q A K V L T F L D S H C E C N E H W L E P L L E R V A E	
Consensus	(201) VIR D R GLIRARLKGA A A VITFLDAHCEC WLEPLL RI	
	251	300
HSGALNAT1.pep	(229)DRRTVVCPIIDVISDDTFEYMAGSDMTYGGFNWKL NFRWYPVPQREMDRR	
HSGALNAT2.pep	(244)DRTRVVSPIIDVINMDNFQYVGASADLKG GFDWNLVFKWDYMTPEQRRSR	
Consensus	(251)DR VV PIIDVI D F YMAAS GGF W L FKW M R	
	301	350
HSGALNAT1.pep	(279)KGDRTL PVRTPTMAGGLEFSIDRDYFQEIGTYDAGMDIWGGENLEISFRIW	
HSGALNAT2.pep	(294)QGNPVAPIKTPTMAGGLEFVMDKFYFEELGKYDMMDVWGGENLEISERVW	
Consensus	(301) G PIKTP IAGGLEF IDK YF EIG YD MDIWGGENLEISFRIW	
	351	400
HSGALNAT1.pep	(329)QCGGTLEIVTCSHVGHVFRKATPYTFPGGTGQIINKNNRRLAEVWMDEFK	
HSGALNAT2.pep	(344)QCGGSLEIIPC SRVGHVFRKQHPYTFPGGSGTVFARNIRRAAEVWMDEYK	
Consensus	(351)QCGGSLEII CS VGHVFRK PYTFPGGSG I KN RR AEVWMDEFK	
	401	450
HSGALNAT1.pep	(379)NFTYIISPGVTKVDYGDISSRVGLRHKLOCKPFSWYLENIYPDSQIPRHY	
HSGALNAT2.pep	(394)NFTYAAVPSARNVPYGNIQSRLELRKKLSCKPFKWYLENVYPELRVPDHQ	
Consensus	(401)NFTY P V YG I SRL LR KL CKPF WYLENIYPD IP H	
	451	500
HSGALNAT1.pep	(429)FSLGEIRNVEITNQCLDNMARKENEKVGIFNCHGMGGNQVFSYTANKEIRT	
HSGALNAT2.pep	(444)DIAFGALQOGTN-CLDTLGHFADGVGVYECHNAGGNQEWALTKEKSVKH	
Consensus	(451) N TN CLD LA VGIF CH GGNQ FA T K IK	
	501	550
HSGALNAT1.pep	(479)DDLCLDVSKLN--GPVTMLKCHHLKGNQLWEYDPVKLTLOHVNSNQCLDK	
HSGALNAT2.pep	(493)MDLCLTVVDRAPGSLIKLQGCRENDSRQKWEQIEGNSKL RHVGSNLC LDS	
Consensus	(501) DLCL V I L C Q WE L HV SN CLD	
	551	584
HSGALNAT1.pep	(527)ATEEDSQVPSIRDCNGSRSQQWLLRNVTLP E I F -	
HSGALNAT2.pep	(543)RTAK-SGGLSVEVCGPALSQQWKETLNLOQ----	
Consensus	(551) T S SI C A SQOW	

FIG. 44

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**FIG. 45**

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